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Ferrara, Napoleone
Fong, Sherman
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Smith, Victoria
Stewart, Timothy A.
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Williams, P. Mickey
Wood, William I.

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Asp	His	Trp	Lys	Ala 110	Leu	Ala	Phe	Arg	Leu 115	Glu	Glu	Glu	Gln	Lys 120
Met	Arg	Pro	Glu	Ile 125	Ala	Gly	Leu	Lys	Pro 130	Ala	Asn	Pro	Pro	Val 135
Leu	Pro	Ala	Pro	Gln 140	Lys	Ala	Asp	Thr	Asp 145	Pro	Glu	Asn	Leu	Pro 150
Glu	Ile	Ser	Ser	Gln 155	Lys	Thr	Gln	Arg	His 160	Ile	Gln	Arg	Gly	Pro 165
Pro	His	Leu	Gln	Ile 170	Arg	Pro	Pro	Ser	Gln 175	Asp	Leu	Lys	Asp	Gly 180
Thr	Gln	Glu	Glu	Ala 185	Thr	Lys	Arg	Gln	Glu 190	Ala	Pro	Val	Asp	Pro 195
Arg	Pro	Glu	Gly	Asp 200	Pro	Gln	Arg	Thr	Val 205	Ile	Ser	Trp	Arg	Gly 210
Ala	Val	Ile	Glu	Pro 215	Glu	Gln	Gly	Thr	Glu 220	Leu	Pro	Ser	Arg	Arg 225
Ala	Glu	Val	Pro	Thr 230	Lys	Pro	Pro	Leu	Pro 235	Pro	Ala	Arg	Thr	Gln 240
Gly	Thr	Pro	Val	His 245	Leu	Asn	Tyr	Arg	Gln 250	Lys	Gly	Val	Ile	Asp 255
Val	Phe	Leu	His	Ala 260	Trp	Lys	Gly	Tyr	Arg 265	Lys	Phe	Ala	Trp	Gly 270
His	Asp	Glu	Leu	Lys 275	Pro	Val	Ser	Arg	Ser 280	Phe	Ser	Glu	Trp	Phe 285
Gly	Leu	Gly	Leu	Thr 290	Leu	Ile	Asp	Ala	Leu 295	Asp	Thr	Met	Trp	Ile 300
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Lys	Lys	Leu	His	Phe 320	Glu	Lys	Asp	Val	Asp 325	Val	Asn	Leu	Phe	Glu 330
Ser	Thr	Ile	Arg	Ile 335	Leu	Gly	Gly	Leu	Leu 340	Ser	Ala	Tyr	His	Leu 345
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Arg	Leu	Met	Pro	Ala 365	Phe	Arg	Thr	Pro	Ser 370	Lys	Ile	Pro	Tyr	Ser 375
Asp	Val	Asn	Ile	Gly 380	Thr	Gly	Val	Ala	His 385	Pro	Pro	Arg	Trp	Thr 390
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Val Glu Lys Val	Thr Gln His Ile His	Gly Leu Ser Gly Lys	Lys		
	425	430	435		
Asp Gly Leu Val	Pro Met Phe Ile Asn	Thr His Ser Gly Leu	Phe		
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Thr His Leu Gly	Val Phe Thr Leu Gly	Ala Arg Ala Asp Ser	Tyr		
	455	460	465		
Tyr Glu Tyr Leu	Leu Lys Gln Trp Ile	Gln Gly Gly Lys Gln	Glu		
	470	475	480		
Thr Gln Leu Leu	Glu Asp Tyr Val Glu	Ala Ile Glu Gly Val	Arg		
	485	490	495		
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	500	505	510		
Gly Glu Leu Ala	His Gly Arg Phe Ser	Ala Lys Met Asp His	Leu		
	515	520	525		
Val Cys Phe Leu	Pro Gly Thr Leu Ala	Leu Gly Val Tyr His	Gly		
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Leu Pro Ala Ser	His Met Glu Leu Ala	Gln Glu Leu Met Glu	Thr		
	545	550	555		
Cys Tyr Gln Met	Asn Arg Gln Met Glu	Thr Gly Leu Ser Pro	Glu		
	560	565	570		
Ile Val His Phe	Asn Leu Tyr Pro Gln	Pro Gly Arg Arg Asp	Val		
	575	580	585		
Glu Val Lys Pro	Ala Asp Arg His Asn	Leu Leu Arg Pro Glu	Thr		
	590	595	600		
Val Glu Ser Leu	Phe Tyr Leu Tyr Arg	Val Thr Gly Asp Arg	Lys		
	605	610	615		
Tyr Gln Asp Trp	Gly Trp Glu Ile Leu	Gln Ser Phe Ser Arg	Phe		
	620	625	630		
Thr Arg Val Pro	Ser Gly Gly Tyr Ser	Ser Ile Asn Asn Val	Gln		
	635	640	645		
Asp Pro Gln Lys	Pro Glu Pro Arg Asp	Lys Met Glu Ser Phe	Phe		
	650	655	660		
Leu Gly Glu Thr	Leu Lys Tyr Leu Phe	Leu Leu Phe Ser Asp	Asp		
	665	670	675		
Pro Asn Leu Leu	Ser Leu Asp Ala Tyr	Val Phe Asn Thr Glu	Ala		
	680	685	690		

His Pro Leu Pro Ile Trp Thr Pro Ala
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<210> 13
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 13
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<210> 14
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<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 14
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<220>
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<223> Synthetic construct.

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<210> 16
<211> 1524
<212> DNA
<213> Homo sapiens

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aaaaaaaaaa	aaaaaaaaaa	aaaaa	1524		

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<210> 17
<211> 327
<212> PRT
<213> Homo sapiens
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<223> Growth factor and cytokines receptors family.

<400> 22

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Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln
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Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly
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<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

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Asn Lys Ile Ser	Glu 95	Leu Lys Asn Gly	Ser 100	Phe Ser Gly Leu	Ser 105
Leu Leu Glu Arg	Leu 110	Asp Leu Arg Asn	Asn 115	Leu Ile Ser Ser	Ile 120
Asp Pro Gly Ala	Phe 125	Trp Gly Leu Ser	Ser 130	Leu Lys Arg Leu	Asp 135
Leu Thr Asn Asn	Arg 140	Ile Gly Cys Leu	Asn 145	Ala Asp Ile Phe	Arg 150
Gly Leu Thr Asn	Leu 155	Val Arg Leu Asn	Leu 160	Ser Gly Asn Leu	Phe 165
Ser Ser Leu Ser	Gln 170	Gly Thr Phe Asp	Tyr 175	Leu Ala Ser Leu	Arg 180
Ser Leu Glu Phe	Gln 185	Thr Glu Tyr Leu	Leu 190	Cys Asp Cys Asn	Ile 195
Leu Trp Met His	Arg 200	Trp Val Lys Glu	Lys 205	Asn Ile Thr Val	Arg 210
Asp Thr Arg Cys	Val 215	Tyr Pro Lys Ser	Leu 220	Gln Ala Gln Pro	Val 225
Thr Gly Val Lys	Gln 230	Glu Leu Leu Thr	Cys 235	Asp Pro Pro Leu	Glu 240
Leu Pro Ser Phe	Tyr 245	Met Thr Pro Ser	His 250	Arg Gln Val Val	Phe 255
Glu Gly Asp Ser	Leu 260	Pro Phe Gln Cys	Met 265	Ala Ser Tyr Ile	Asp 270
Gln Asp Met Gln	Val 275	Leu Trp Tyr Gln	Asp 280	Gly Arg Ile Val	Glu 285
Thr Asp Glu Ser	Gln 290	Gly Ile Phe Val	Glu 295	Lys Asn Met Ile	His 300
Asn Cys Ser Leu	Ile 305	Ala Ser Ala Leu	Thr 310	Ile Ser Asn Ile	Gln 315
Ala Gly Ser Thr	Gly 320	Asn Trp Gly Cys	His 325	Val Gln Thr Lys	Arg 330
Gly Asn Asn Thr	Arg 335	Thr Val Asp Ile	Val 340	Val Leu Glu Ser	Ser 345
Ala Gln Tyr Cys	Pro 350	Pro Glu Arg Val	Val 355	Asn Asn Lys Gly	Asp 360
Phe Arg Trp Pro	Arg 365	Thr Leu Ala Gly	Ile 370	Thr Ala Tyr Leu	Gln 375
Cys Thr Arg Asn	Thr	His Gly Ser Gly	Ile	Tyr Pro Gly Asn	Pro

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Gln Asp Glu Arg	Lys Ala Trp Arg Arg	Cys Asp Arg Gly Gly	Phe		
	395	400	405		
Trp Ala Asp Asp	Asp Tyr Ser Arg Cys	Gln Tyr Ala Asn Asp	Val		
	410	415	420		
Thr Arg Val Leu	Tyr Met Phe Asn Gln	Met Pro Leu Asn Leu	Thr		
	425	430	435		
Asn Ala Val Ala	Thr Ala Arg Gln Leu	Leu Ala Tyr Thr Val	Glu		
	440	445	450		
Ala Ala Asn Phe	Ser Asp Lys Met Asp	Val Ile Phe Val Ala	Glu		
	455	460	465		
Met Ile Glu Lys	Phe Gly Arg Phe Thr	Lys Glu Glu Lys Ser	Lys		
	470	475	480		
Glu Leu Gly Asp	Val Met Val Asp Ile	Ala Ser Asn Ile Met	Leu		
	485	490	495		
Ala Asp Glu Arg	Val Leu Trp Leu Ala	Gln Arg Glu Ala Lys	Ala		
	500	505	510		
Cys Ser Arg Ile	Val Gln Cys Leu Gln	Arg Ile Ala Thr Tyr	Arg		
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Leu Ala Gly Gly	Ala His Val Tyr Ser	Thr Tyr Ser Pro Asn	Ile		
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Ala Leu Glu Ala	Tyr Val Ile Lys Ser	Thr Gly Phe Thr Gly	Met		
	545	550	555		
Thr Cys Thr Val	Phe Gln Lys Val Ala	Ala Ser Asp Arg Thr	Gly		
	560	565	570		
Leu Ser Asp Tyr	Gly Arg Arg Asp Pro	Glu Gly Asn Leu Asp	Lys		
	575	580	585		
Gln Leu Ser Phe	Lys Cys Asn Val Ser	Asn Thr Phe Ser Ser	Leu		
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Ser

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 <212> DNA
 <213> Artificial
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 <221> Artificial Sequence
 <222> 1-24

<223> Synthetic construct

<400> 25

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<210> 26

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 26

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<210> 27

<211> 50

<212> DNA

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<222> 1-50

<223> Synthetic construct.

<400> 27

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<210> 28

<211> 683

<212> DNA

<213> Homo sapiens

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gcagaggctt cgtgacggag ttatcagaga cattgagagg caaattcgga 150

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 <212> PRT
 <213> Homo sapiens

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 <221> sig_peptide
 <222> 1-21
 <223> Signal peptide.

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 35 40 45
 Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile
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 Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala
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 <211> 2128
 <212> DNA
 <213> Homo sapiens

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<211> 335

<212> PRT

<213> Homo sapiens

<400> 33

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Ser	Leu	Ala	Gln	Val	Asn	Leu	Ser	Pro	Phe	Ser	His	Pro	Lys	Val
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His	Met	Asp	Pro	Asn	Tyr	Cys	His	Pro	Ser	Thr	Ser	Leu	His	Leu
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Cys	Ser	Leu	Ala	Trp	Ser	Phe	Thr	Arg	Leu	Leu	His	Pro	Pro	Leu
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Ser	Pro	Gly	Ile	Ser	Gln	Val	Val	Lys	Asp	His	Val	Thr	Lys	Pro
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Thr	Ala	Met	Ala	Gln	Gly	Arg	Val	Ala	His	Leu	Ile	Glu	Trp	Lys
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Gly	Trp	Ser	Lys	Pro	Ser	Asp	Ser	Pro	Ala	Ala	Leu	Glu	Ser	Ala
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Phe	Ser	Ser	Tyr	Ser	Asp	Leu	Ser	Glu	Gly	Glu	Gln	Glu	Ala	Arg
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Phe	Ala	Ala	Gly	Val	Ala	Glu	Gln	Phe	Ala	Ile	Ala	Glu	Ala	Lys
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Leu	Arg	Ala	Trp	Ser	Ser	Val	Asp	Gly	Glu	Asp	Ser	Thr	Asp	Asp
				155					160					165

Ser	Tyr	Asp	Glu	Asp	Phe	Ala	Gly	Gly	Met	Asp	Thr	Asp	Met	Ala
				170					175					180

Gly	Gln	Leu	Pro	Leu	Gly	Pro	His	Leu	Gln	Asp	Leu	Phe	Thr	Gly
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His	Arg	Phe	Ser	Arg	Pro	Val	Arg	Gln	Gly	Ser	Val	Glu	Pro	Glu
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Ser	Asp	Cys	Ser	Gln	Thr	Val	Ser	Pro	Asp	Thr	Leu	Cys	Ser	Ser
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Leu	Cys	Ser	Leu	Glu	Asp	Gly	Leu	Leu	Gly	Ser	Pro	Ala	Arg	Leu
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Pro	Ser	Arg	Glu	Ser	Ala	Phe	Arg	Ser	Leu	Gly	Pro	Leu	Glu	Ala
			260						265					270
Gln	Asp	Ser	Leu	Tyr	Asn	Ser	Pro	Leu	Thr	Glu	Ser	Cys	Leu	Ser
			275						280					285
Pro	Ala	Glu	Glu	Glu	Pro	Ala	Pro	Cys	Lys	Asp	Cys	Gln	Pro	Leu
			290						295					300
Cys	Pro	Pro	Leu	Thr	Gly	Ser	Trp	Glu	Arg	Gln	Arg	Gln	Ala	Ser
			305						310					315
Asp	Leu	Ala	Ser	Ser	Gly	Val	Val	Ser	Leu	Asp	Glu	Asp	Glu	Ala
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 <212> DNA
 <213> Artificial

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 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct

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 <223> Synthetic construct.

<400> 35
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 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 36

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<211> 334
<212> PRT
<213> Homo sapiens

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35 40 45
Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu 60
50 55 60
Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu 75
65 70 75
Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn 90
80 85 90
Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr 105
95 100 105
Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val 120
110 115 120
Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser 135
125 130 135
Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr 150
140 145 150
Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser 165
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Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val 180
170 175 180
Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser 195
185 190 195

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<211> 263

<212> PRT

<213> Homo sapiens

<400> 43

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				20					25					30

Thr	Gln	Ile	Leu	Thr	Gly	Lys	Glu	Leu	Arg	Val	Ala	Thr	Gln	Glu
				35					40					45

Lys	Glu	Gly	Ser	Ser	Gly	Arg	Cys	Met	Leu	Thr	Leu	Leu	Gly	Leu
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Gly	Asp	Asn	Tyr	Arg	Gly	Gln	Gly	Ser	Ser	Trp	Gly	Ser	Gly	Gly	
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Gly	Asp	Ala	Val	Gly	Gly	Val	Asn	Thr	Val	Asn	Ser	Glu	Thr	Ser	
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Pro	Gly	Met	Phe	Asn	Phe	Asp	Thr	Phe	Trp	Lys	Asn	Phe	Lys	Ser	
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Lys	Leu	Gly	Phe	Ile	Asn	Trp	Asp	Ala	Ile	Asn	Lys	Asp	Gln	Arg	
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 <212> DNA
 <213> Homo sapiens

<400> 53
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<210> 54

<211> 280

<212> PRT

<213> Homo sapiens

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 acaacagacc tgggttttcc tcgaagtgcc cttccaccct cctgcccgtg 3050
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<210> 58

<211> 1115

<212> PRT

<213> Homo sapiens

<400> 58

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				20					25					30	
Asp	Leu	Asn	Glu	Val	Pro	Gln	Val	Thr	Val	Gln	Pro	Ala	Ser	Thr	
				35					40					45	
Val	Gln	Lys	Pro	Gly	Gly	Thr	Val	Ile	Leu	Gly	Cys	Val	Val	Glu	
				50					55					60	
Pro	Pro	Arg	Met	Asn	Val	Thr	Trp	Arg	Leu	Asn	Gly	Lys	Glu	Leu	
				65					70					75	
Asn	Gly	Ser	Asp	Asp	Ala	Leu	Gly	Val	Leu	Ile	Thr	His	Gly	Thr	
				80					85					90	
Leu	Val	Ile	Thr	Ala	Leu	Asn	Asn	His	Thr	Val	Gly	Arg	Tyr	Gln	
				95					100					105	
Cys	Val	Ala	Arg	Met	Pro	Ala	Gly	Ala	Val	Ala	Ser	Val	Pro	Ala	
				110					115					120	
Thr	Val	Thr	Leu	Ala	Asn	Leu	Gln	Asp	Phe	Lys	Leu	Asp	Val	Gln	
				125					130					135	
His	Val	Ile	Glu	Val	Asp	Glu	Gly	Asn	Thr	Ala	Val	Ile	Ala	Cys	
				140					145					150	
His	Leu	Pro	Glu	Ser	His	Pro	Lys	Ala	Gln	Val	Arg	Tyr	Ser	Val	
				155					160					165	
Lys	Gln	Glu	Trp	Leu	Glu	Ala	Ser	Arg	Gly	Asn	Tyr	Leu	Ile	Met	
				170					175					180	
Pro	Ser	Gly	Asn	Leu	Gln	Ile	Val	Asn	Ala	Ser	Gln	Glu	Asp	Glu	
				185					190					195	
Gly	Met	Tyr	Lys	Cys	Ala	Ala	Tyr	Asn	Pro	Val	Thr	Gln	Glu	Val	
				200					205					210	
Lys	Thr	Ser	Gly	Ser	Ser	Asp	Arg	Leu	Arg	Val	Arg	Arg	Ser	Thr	
				215					220					225	
Ala	Glu	Ala	Ala	Arg	Ile	Ile	Tyr	Pro	Pro	Glu	Ala	Gln	Thr	Ile	
				230					235					240	
Ile	Val	Thr	Lys	Gly	Gln	Ser	Leu	Ile	Leu	Glu	Cys	Val	Ala	Ser	
				245					250					255	
Gly	Ile	Pro	Pro	Pro	Arg	Val	Thr	Trp	Ala	Lys	Asp	Gly	Ser	Ser	
				260					265					270	

Arg Pro Lys Pro	560	Ile Met Ala Ser	565	Lys Glu Gln Gln Ile Gln	570
	575		580		585
Arg Asp Asp Pro	Gly Ala Ser Pro Gln	Ser Ser Ser Gln Pro Asp			
	590		595		600
His Gly Arg Leu	Ser Pro Pro Glu Ala	Pro Asp Arg Pro Thr Ile			
	605		610		615
Ser Thr Ala Ser	Glu Thr Ser Val Tyr	Val Thr Trp Ile Pro Arg			
	620		625		630
Gly Asn Gly Gly	Phe Pro Ile Gln Ser	Phe Arg Val Glu Tyr Lys			
	635		640		645
Lys Leu Lys Lys	Val Gly Asp Trp Ile	Leu Ala Thr Ser Ala Ile			
	650		655		660
Pro Pro Ser Arg	Leu Ser Val Glu Ile	Thr Gly Leu Glu Lys Gly			
	665		670		675
Thr Ser Tyr Lys	Phe Arg Val Arg Ala	Leu Asn Met Leu Gly Glu			
	680		685		690
Ser Glu Pro Ser	Ala Pro Ser Arg Pro	Tyr Val Val Ser Gly Tyr			
	695		700		705
Ser Gly Arg Val	Tyr Glu Arg Pro Val	Ala Gly Pro Tyr Ile Thr			
	710		715		720
Phe Thr Asp Ala	Val Asn Glu Thr Thr	Ile Met Leu Lys Trp Met			
	725		730		735
Tyr Ile Pro Ala	Ser Asn Asn Asn Thr	Pro Ile His Gly Phe Tyr			
	740		745		750
Ile Tyr Tyr Arg	Pro Thr Asp Ser Asp	Asn Asp Ser Asp Tyr Lys			
	755		760		765
Lys Asp Met Val	Glu Gly Asp Lys Tyr	Trp His Ser Ile Ser His			
	770		775		780
Leu Gln Pro Glu	Thr Ser Tyr Asp Ile	Lys Met Gln Cys Phe Asn			
	785		790		795
Glu Gly Gly Glu	Ser Glu Phe Ser Asn	Val Met Ile Cys Glu Thr			
	800		805		810
Lys Ala Arg Lys	Ser Ser Gly Gln Pro	Gly Arg Leu Pro Pro Pro			
	815		820		825
Thr Leu Ala Pro	Pro Gln Pro Pro Leu	Pro Glu Thr Ile Glu Arg			
	830		835		840
Pro Val Gly Thr	Gly Ala Met Val Ala	Arg Ser Ser Asp Leu Pro			
	845		850		855

	260		265		270
Ser Asp Thr Leu	Ile Arg Arg Val Leu	Glu Val Ser Gln Ala	Pro		
	275		280		285
Val Ile Phe Ser	His Ser Ala Ala Arg	Ala Val Cys Asp Asn	Leu		
	290		295		300
Leu Asn Val Pro	Asp Asp Ile Leu Gln	Leu Leu Lys Asn Gly	Gly		
	305		310		315
Ile Val Met Val	Thr Leu Ser Met Gly	Val Leu Gln Cys Asn	Leu		
	320		325		330
Leu Ala Asn Val	Ser Thr Val Ala Asp	His Phe Asp His Ile	Arg		
	335		340		345
Ala Val Ile Gly	Ser Glu Phe Ile Gly	Ile Gly Gly Asn Tyr	Asp		
	350		355		360
Gly Thr Gly Arg	Phe Pro Gln Gly Leu	Glu Asp Val Ser Thr	Tyr		
	365		370		375
Pro Val Leu Ile	Glu Glu Leu Leu Ser	Arg Xaa Trp Ser Glu	Glu		
	380		385		390
Glu Leu Gln Gly	Val Leu Arg Gly Asn	Leu Leu Arg Val Phe	Arg		
	395		400		405
Gln Val Glu Lys	Val Arg Glu Glu Ser	Arg Ala Gln Ser Pro	Val		
	410		415		420
Glu Ala Glu Phe	Pro Tyr Gly Gln Leu	Ser Thr Ser Cys His	Ser		
	425		430		435
His Leu Val Pro	Gln Asn Gly His Gln	Ala Thr His Leu Glu	Val		
	440		445		450
Thr Lys Gln Pro	Thr Asn Arg Val Pro	Trp Arg Ser Ser Asn	Ala		
	455		460		465
Ser Pro Tyr Leu	Val Pro Gly Leu Val	Ala Ala Ala Thr Ile	Pro		
	470		475		480
Thr Phe Thr Gln	Trp Leu Cys				
	485				

<210> 64

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 64

ccttcacctg cagtacacca tgggc 25

<210> 65

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 65

gtcacacaca gctctggcag ctgag 25

<210> 66

<211> 47

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-47

<223> Synthetic construct.

<400> 66

ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67

<211> 1564

<212> DNA

<213> Homo sapiens

<400> 67

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acaatgagga ggagaatgag gatgctcgct ctatggcagc agctgctgca 550
tccctcgggg gaccccgagc aaacacagtc ctggagcgtg tggaaggtgc 600

Pro Met Pro Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu
65 70 75
Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val
80 85 90
Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu Leu Leu Tyr
95 100 105
Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys Pro Asp
110 115 120
Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp Ala
125 130 135
Arg Ser Met Ala Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala
140 145 150
Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys
155 160 165
Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys
170 175 180
Met Leu Ser

<210> 69
<211> 3170
<212> DNA
<213> Homo sapiens

<400> 69
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tccctttgca ttcccacccc tccgggcttt gcgctcttct ggggaccccc 200
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<211> 259

<212> PRT

<213> Homo sapiens

<400> 70

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Leu Leu Ala Ala Val Leu Met Val Glu Ser Ser Gln Ile Gly Ser
20 25 30

Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly Glu
35 40 45

Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly
50 55 60

Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala
65 70 75

Tyr Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys
80 85 90

His Ser Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg
95 100 105

Lys Lys Lys Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr
110 115 120

Arg Cys Asn Asn Gly Ile Cys Ile Pro Val Thr Glu Ser Ile Leu
125 130 135

Thr Pro His Ile Pro Ala Leu Asp Gly Thr Arg His Arg Asp Arg
140 145 150

Asn His Gly His Tyr Ser Asn His Asp Leu Gly Trp Gln Asn Leu
155 160 165

Gly Arg Pro His Thr Lys Met Ser His Ile Lys Gly His Glu Gly
170 175 180

Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly Phe Cys Cys
185 190 195

Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu His Gln
200 205 210

Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly Leu
215 220 225

Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys
230 235 240

Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val
245 250 255

Cys Gln Lys Ile

<210> 71
<211> 1809
<212> DNA
<213> Homo sapiens

<400> 71
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<210> 72
 <211> 363
 <212> PRT
 <213> Homo sapiens

<400> 72

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Cys	Ser	Phe	Ile	Pro	Leu	Leu	Lys	Ser	Ser	Val	Leu	Gly	Ser	Gly
				20					25					30
Phe	Gly	Glu	Leu	Ala	Pro	Pro	Lys	Met	Ala	Asn	Ile	Thr	Ser	Ser
				35					40					45
Gln	Ile	Leu	Asp	Gln	Leu	Lys	Ala	Pro	Ser	Leu	Gly	Gln	Phe	Thr
				50					55					60
Thr	Thr	Pro	Ser	Thr	Gln	Gln	Asn	Ser	Thr	Ser	His	Pro	Thr	Thr
				65					70					75
Thr	Thr	Ser	Trp	Asp	Leu	Lys	Pro	Pro	Thr	Ser	Gln	Ser	Ser	Val
				80					85					90
Leu	Ser	His	Leu	Asp	Phe	Lys	Ser	Gln	Pro	Glu	Pro	Ser	Pro	Val
				95					100					105
Leu	Ser	Gln	Leu	Ser	Gln	Arg	Gln	Gln	His	Gln	Ser	Gln	Ala	Val
				110					115					120
Thr	Val	Pro	Pro	Pro	Gly	Leu	Glu	Ser	Phe	Pro	Ser	Gln	Ala	Lys
				125					130					135
Leu	Arg	Glu	Ser	Thr	Pro	Gly	Asp	Ser	Pro	Ser	Thr	Val	Asn	Lys
				140					145					150
Leu	Leu	Gln	Leu	Pro	Ser	Thr	Thr	Ile	Glu	Asn	Ile	Ser	Val	Ser
				155					160					165
Val	His	Gln	Pro	Gln	Pro	Lys	His	Ile	Lys	Leu	Ala	Lys	Arg	Arg
				170					175					180
Ile	Pro	Pro	Ala	Ser	Lys	Ile	Pro	Ala	Ser	Ala	Val	Glu	Met	Pro
				185					190					195
Gly	Ser	Ala	Asp	Val	Thr	Gly	Leu	Asn	Val	Gln	Phe	Gly	Ala	Leu
				200					205					210
Glu	Phe	Gly	Ser	Glu	Pro	Ser	Leu	Ser	Glu	Phe	Gly	Ser	Ala	Pro
				215					220					225

Ser Ser Glu Asn	Ser Asn Gln Ile Pro Ile Ser Leu Tyr Ser Lys	230	235	240
Ser Leu Ser Glu	Pro Leu Asn Thr Ser Leu Ser Met Thr Ser Ala	245	250	255
Val Gln Asn Ser	Thr Tyr Thr Thr Ser Val Ile Thr Ser Cys Ser	260	265	270
Leu Thr Ser Ser	Ser Leu Asn Ser Ala Ser Pro Val Ala Met Ser	275	280	285
Ser Ser Tyr Asp	Gln Ser Ser Val His Asn Arg Ile Pro Tyr Gln	290	295	300
Ser Pro Val Ser	Ser Ser Glu Ser Ala Pro Gly Thr Ile Met Asn	305	310	315
Gly His Gly Gly	Gly Arg Ser Gln Gln Thr Leu Asp Ser Lys Tyr	320	325	330
Ser Ser Lys Leu	Leu Leu Ser Trp Leu Val Pro Thr Lys Gln Arg	335	340	345
Lys Arg Ile Ala	His Val Met Trp Lys Thr Pro Val Gly Gln Trp	350	355	360
Leu Ile Arg				

<210> 73
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 73
 aattcatggc aaatatttcc cttccc 26

<210> 74
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 74
 tggtaaaactg gcccaaactc gg 22

<210> 75
 <211> 50

<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-50
<223> Synthetic construct

<400> 75
ttaaagtcac ccgtccttgg ctcaggattt ggagagcttg caccaccaa 50

<210> 76
<211> 1989
<212> DNA
<213> Homo sapiens

<400> 76
gccgagtgagg acaaagcctg gggctgggag ggggcatgg cgctgccatc 50
ccgaatcctg ctttggaac ttgtgcttct gcagagctct gctgttctcc 100
tgactcagc ggtggaggag acggaacggg ggtgtacac ctgcaacctg 150
caccatcact actgccacct ctacgagagc ctggccgtcc gcctggagggt 200
caccgacggc ccccgggcca ccccgcccta ctgggacggc gagaaggagg 250
tgctggcggg ggcgcgcggc gacccgcgc ttctgacctg cgtgaaccgc 300
gggcacgtgt ggaccgacgg gacgtggag gaggctcaac aggtgggtgca 350
ctgggaccgg cagccggccg gggccccgca cgaccgcgcg gaccgcctgc 400
tggacctcta cgcgtcgggc gagcgcgcgc cctacgggcc ctttttctg 450
cgcgaccgcg tggctgtggg cgcggatgcc tttgagcgcg gtgacttctc 500
actgcgtatc gagccgctgg aggtcgccga cgagggcacc tactcctgcc 550
acctgcacca ccattactgt ggctgcacg aacgccgcgt cttccacctg 600
acggtcgccg aaccccaacg ggagccggcc ccccggggct ctccgggcaa 650
cggctccagc cacagcggcg cccagggccc agacccaca ctggcgcgcg 700
gccacaacgt catcaatgtc atcgtccccg agagccgagc ccacttcttc 750
cagcagctgg gctacgtgct ggccacgctg ctgctcttca tcctgtact 800
ggtcactgtc ctctggccg cccgcaggcg ccgcggaggc tacgaatact 850
cggaccagaa gtcgggaaag tcaaagggga aggatgttaa cttggcggag 900
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gctagattac aaaaacaaca tcctgaagga gagggcggag ctggccca 1000
gccccctgcc tgccaagtac atcgacctag acaaagggtt ccggaaggag 1050

aactgcaaat agggaggccc tgggctcctg gctgggccag cagctgcacc 1100
 tctoctgtct gtgctcctcg gggcatctcc tgatgtccg gggctcacc 1150
 cccttccagc ggctgggtccc gctttcctgg aatttggcct gggcgtatgc 1200
 agaggccgcc tccacacccc tccccaggg gcttggtggc agcatagccc 1250
 ccacccctgc ggcttttgc caggggtggc cctgcccacc cctggcacia 1300
 ccaaaatccc actgatgcc atcatgccct cagacccttc tgggctctgc 1350
 ccgctggggg cctgaagaca ttcttgagg aactcccat cagaacctgg 1400
 cagccccaaa actggggtca gcctcagggc aggagtcca ctctccagg 1450
 gctctgctcg tccggggctg ggagatgttc ctggaggagg aactcccat 1500
 cagaacttgg cagccttgaa gttggggtca gcctcggcag gactcccat 1550
 cctctggggg tgctgctgc caccaagagc tccccacct gtaccacat 1600
 gtgggactcc aggcaccatc tgttctccc agggacctgc tgacttgaat 1650
 gccagccctt gctcctctgt gttgctttgg gccacctggg gctgcacccc 1700
 ctgccctttc tctgccccat ccctacccta gccttgctct cagccacctt 1750
 gatagtact gggctccctg tgacttctga ccctgacacc cctcccttgg 1800
 actctgcctg ggctggagtc tagggctggg gctacatttg gcttctgtac 1850
 tggctgagga caggggaggg agtgaagttg gtttggggtg gcctgtgttg 1900
 ccactctcag cccccacat ttgcatctgc tgggtggacct gccaccatca 1950
 caataaagtc cccatctgat ttttaaaaaa aaaaaaaaaa 1989

<210> 77
 <211> 341
 <212> PRT
 <213> Homo sapiens

<400> 77
 Met Ala Leu Pro Ser Arg Ile Leu Leu Trp Lys Leu Val Leu Leu
 1 5 10 15
 Gln Ser Ser Ala Val Leu Leu His Ser Ala Val Glu Glu Thr Asp
 20 25 30
 Ala Gly Leu Tyr Thr Cys Asn Leu His His His Tyr Cys His Leu
 35 40 45
 Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Gly Pro Pro
 50 55 60
 Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Ala Val
 65 70 75

Ala Arg Gly Ala	Pro Ala Leu Leu Thr	Cys Val Asn Arg Gly His	80	85	90
Val Trp Thr Asp	Arg His Val Glu Glu	Ala Gln Gln Val Val His	95	100	105
Trp Asp Arg Gln	Pro Pro Gly Val Pro	His Asp Arg Ala Asp Arg	110	115	120
Leu Leu Asp Leu	Tyr Ala Ser Gly Glu	Arg Arg Ala Tyr Gly Pro	125	130	135
Leu Phe Leu Arg	Asp Arg Val Ala Val	Gly Ala Asp Ala Phe Glu	140	145	150
Arg Gly Asp Phe	Ser Leu Arg Ile Glu	Pro Leu Glu Val Ala Asp	155	160	165
Glu Gly Thr Tyr	Ser Cys His Leu His	His His Tyr Cys Gly Leu	170	175	180
His Glu Arg Arg	Val Phe His Leu Thr	Val Ala Glu Pro His Ala	185	190	195
Glu Pro Pro Pro	Arg Gly Ser Pro Gly	Asn Gly Ser Ser His Ser	200	205	210
Gly Ala Pro Gly	Pro Asp Pro Thr Leu	Ala Arg Gly His Asn Val	215	220	225
Ile Asn Val Ile	Val Pro Glu Ser Arg	Ala His Phe Phe Gln Gln	230	235	240
Leu Gly Tyr Val	Leu Ala Thr Leu Leu	Leu Phe Ile Leu Leu Leu	245	250	255
Val Thr Val Leu	Leu Ala Ala Arg Arg	Arg Arg Gly Gly Tyr Glu	260	265	270
Tyr Ser Asp Gln	Lys Ser Gly Lys Ser	Lys Gly Lys Asp Val Asn	275	280	285
Leu Ala Glu Phe	Ala Val Ala Ala Gly	Asp Gln Met Leu Tyr Arg	290	295	300
Ser Glu Asp Ile	Gln Leu Asp Tyr Lys	Asn Asn Ile Leu Lys Glu	305	310	315
Arg Ala Glu Leu	Ala His Ser Pro Leu	Pro Ala Lys Tyr Ile Asp	320	325	330
Leu Asp Lys Gly	Phe Arg Lys Glu Asn	Cys Lys	335	340	

<210> 78
 <211> 2243
 <212> DNA
 <213> Homo sapiens

Tyr Leu Ala Val	Ala Ser Thr Val	Pro Ser Met Leu Cys Leu Val	110	115	120
Ala Asn Phe Leu	Leu Val Asn Arg Val	Ala Val His Ile Arg Val	125	130	135
Leu Ala Ser Leu	Thr Val Ile Leu Ala	Ile Phe Met Val Ile Thr	140	145	150
Ala Leu Val Lys	Val Asp Thr Ser Ser	Trp Thr Arg Gly Phe Phe	155	160	165
Ala Val Thr Ile	Val Cys Met Val Ile	Leu Ser Gly Ala Ser Thr	170	175	180
Val Phe Ser Ser	Ser Ile Tyr Gly Met	Thr Gly Ser Phe Pro Met	185	190	195
Arg Asn Ser Gln	Ala Leu Ile Ser Gly	Gly Ala Met Gly Gly Thr	200	205	210
Val Ser Ala Val	Ala Ser Leu Val Asp	Leu Ala Ala Ser Ser Asp	215	220	225
Val Arg Asn Ser	Ala Leu Ala Phe Phe	Leu Thr Ala Thr Ile Phe	230	235	240
Leu Val Leu Cys	Met Gly Leu Tyr Leu	Leu Leu Ser Arg Leu Glu	245	250	255
Tyr Ala Arg Tyr	Tyr Met Arg Pro Val	Leu Ala Ala His Val Phe	260	265	270
Ser Gly Glu Glu	Glu Leu Pro Gln Asp	Ser Leu Ser Ala Pro Ser	275	280	285
Val Ala Ser Arg	Phe Ile Asp Ser His	Thr Pro Pro Leu Arg Pro	290	295	300
Ile Leu Lys Lys	Thr Ala Ser Leu Gly	Phe Cys Val Thr Tyr Val	305	310	315
Phe Phe Ile Thr	Ser Leu Ile Tyr Pro	Ala Val Cys Thr Asn Ile	320	325	330
Glu Ser Leu Asn	Lys Gly Ser Gly Ser	Leu Trp Thr Thr Lys Phe	335	340	345
Phe Ile Pro Leu	Thr Thr Phe Leu Leu	Tyr Asn Phe Ala Asp Leu	350	355	360
Cys Gly Arg Gln	Leu Thr Ala Trp Ile	Gln Val Pro Gly Pro Asn	365	370	375
Ser Lys Ala Leu	Pro Gly Phe Val Leu	Leu Arg Thr Cys Leu Ile	380	385	390
Pro Leu Phe Val	Leu Cys Asn Tyr Gln	Pro Arg Val His Leu Lys			

<212> DNA
<213> Homo sapiens

<400> 83

gacagtggag ggcagtggag aggaccgcgc tgtcctgctg tcaccaagag 50
ctggagacac catctccac cgagagtcac ggccccattg gccctgcacc 100
tcctcgtcct cgtccccatc ctctcagcc tggcggcctc ccaggactgg 150
aaggctgaac gcagccaaga ccccttcgag aaatgcatgc aggatcctga 200
ctatgagcag ctgctcaagg tggcgacctg ggggctcaat cggaccctga 250
agccccagag ggtgattgtg gttggcgctg gtgtggccgg gctggtggcc 300
gccaagggtgc tcagcgatgc tggacacaag gtcaccatcc tggaggcaga 350
taacaggatc gggggccgca tcttcaccta ccgggaccag aacacgggct 400
ggattgggga gctgggagcc atgcgcatgc ccagctctca caggatcctc 450
cacaagctct gccaggcctt ggggctcaac ctgaccaagt tcaccagta 500
cgacaagaac acgtggacgg aggtgcacga agtgaagctg cgcaactatg 550
tggcggagaa ggtgcccag aagctgggct acgccttgcg tccccaggaa 600
aaggggcact cgcccgaaga catctaccag atggctctca accaggccct 650
caaagacctc aaggcactgg gctgcagaaa ggcgatgaag aagtttgaaa 700
ggcacacgct cttggaatat cttctcgggg aggggaacct gagccggccg 750
gccgtgcagc ttctgggaga cgtgatgtcc gaggatggct tcttctatct 800
cagcttcgcc gagggccctc gggccacag ctgcctcagc gacagactcc 850
agtacagccg catcgtgggt ggctgggacc tgctgccgag cgcgctgctg 900
agctcgtgt cggggttgt gctgttgaa gcgcccgtgg tggcgatgac 950
ccagggaccg cacgatgtgc acgtgcagat cgagacctct cccccggcgc 1000
ggaatctgaa ggtgctgaag gccgacgtgg tgctgctgac ggcgagcgga 1050
ccggcggtga agcgcatcac cttctcgccg ccgctgcccc gccacatgca 1100
ggaggcgctg cggaggctgc actacgtgcc ggccaccaag gtgttcctaa 1150
gcttcgcag gcccttctgg cgcgaggagc acattgaagg cggccactca 1200
aacacogatc gcccgctcgc catgattttc taccgcccgc cgcgcgaggg 1250
cgcgctgctg ctggcctcgt acacgtggtc ggacgcggcg gcagcgttcg 1300
ccggcttgag ccgggaagag gcgttgcgct tggcgctcga cgacgtggcg 1350

455	460	465
Lys Asp Asp Trp Thr Val Pro Tyr Gly	Arg Ile Tyr Phe Ala Gly	
470	475	480
Glu His Thr Ala Tyr Pro His Gly Trp	Val Glu Thr Ala Val Lys	
485	490	495
Ser Ala Leu Arg Ala Ala Ile Lys Ile	Asn Ser Arg Lys Gly Pro	
500	505	510
Ala Ser Asp Thr Ala Ser Pro Glu Gly	His Ala Ser Asp Met Glu	
515	520	525
Gly Gln Gly His Val His Gly Val Ala	Ser Ser Pro Ser His Asp	
530	535	540
Leu Ala Lys Glu Glu Gly Ser His Pro	Pro Val Gln Gly Gln Leu	
545	550	555
Ser Leu Gln Asn Thr Thr His Thr Arg	Thr Ser His	
560	565	

<210> 85
 <211> 3316
 <212> DNA
 <213> Homo sapiens

<400> 85
 ctgacatggc ctgactcggg acagctcaga gcagggcaga actggggaca 50
 ctctgggccc gccttctgcc tgcattggacg ctctgaagcc accctgtctc 100
 tggaggaacc acgagcggg gaagaaggac agggactcgt gtggcaggaa 150
 gaactcagag ccgggaagcc cccattcact agaagcactg agagatgcgg 200
 cccctcgcga gggctcgaat ttctctgtgc tgttcacaaa gatgcttttt 250
 atctttaact ttttgttttc ccacttccg accccggcgt tgatctgcat 300
 cctgacattt ggagctgcca ttttcttggt gctgatcacc agacctcaac 350
 ccgtcttacc ttttcttgac ctgaacaatc agtctgtggg aattgaggga 400
 ggagcacgga agggggtttc ccagaagaac aatgacctaa caagttgctg 450
 cttctcagat gccaagacta tgtatgaggt tttccaaaga ggactcgtctg 500
 tgtctgacaa tgggccctgc ttgggatata gaaaacaaa ccagccctac 550
 agatggctat cttacaaaca ggtgtctgat agagcagagt acctgggttc 600
 ctgtctcttg cataaagggt ataatcatc accagaccag tttgtcggca 650
 tctttgtcga gaataggcca gaggatga tctccgaatt ggcttggtac 700
 acgtactcta tggtagctgt acctctgtat gacaccttg gaccagaagc 750

ctcttgacac caacattgaa agcaaagcga ggagagcttt ccaaatactt 2250
 tgggacccaa attgacagcc tgtatgagca catccaggat taggataagg 2300
 tacttaagta cctgccggcc cactgtgcac tgcttgtgag aaaatggatt 2350
 aaaaactatt cttacatttg ttttgccttt cctcctattt ttttttaacc 2400
 tgttaaactc taaagccata gcttttggtt tatattgaga catataatgt 2450
 gtaaacttag ttcccaaata aatcaatcct gtctttccca tcttcgatgt 2500
 tgctaataatt aaggcttcag ggctactttt atcaacatgc ctgtcttcaa 2550
 gatcccagtt tatgttctgt gtccttcctc atgatttcca accttaatac 2600
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 aattcatgtt ttctagccac tccacaaacc actaaaattt tagtttttagc 2800
 ctatcactca tgtcaatcat atctatgaga caaatgtctc cgatgctctt 2850
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 cagtaggaac tggggagtaa atctgttccc tacagtttgc tgctgagctg 3050
 gaagctgtgg gggaaggagt tgacaggtgg gccagtgaa cttttccagt 3100
 aatgaagca agcactgaat aaaaacctcc tgaactggga acaaagatct 3150
 acaggcaagc aagatgccca cacaacaggc ttattttctg tgaaggaacc 3200
 aactgatctc cccaccctt ggattagagt tctgctcta ccttaccac 3250
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<210> 86

<211> 739

<212> PRT

<213> Homo sapiens

<400> 86

Met Asp Ala Leu Lys Pro Pro Cys Leu Trp Arg Asn His Glu Arg
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Gly Lys Lys Asp Arg Asp Ser Cys Gly Arg Lys Asn Ser Glu Pro
 20 25 30

Gly	Ser	Pro	His	Ser 35	Leu	Glu	Ala	Leu	Arg 40	Asp	Ala	Ala	Pro	Ser 45
Gln	Gly	Leu	Asn	Phe 50	Leu	Leu	Leu	Phe	Thr 55	Lys	Met	Leu	Phe	Ile 60
Phe	Asn	Phe	Leu	Phe 65	Ser	Pro	Leu	Pro	Thr 70	Pro	Ala	Leu	Ile	Cys 75
Ile	Leu	Thr	Phe	Gly 80	Ala	Ala	Ile	Phe	Leu 85	Trp	Leu	Ile	Thr	Arg 90
Pro	Gln	Pro	Val	Leu 95	Pro	Leu	Leu	Asp	Leu 100	Asn	Asn	Gln	Ser	Val 105
Gly	Ile	Glu	Gly	Gly 110	Ala	Arg	Lys	Gly	Val 115	Ser	Gln	Lys	Asn	Asn 120
Asp	Leu	Thr	Ser	Cys 125	Cys	Phe	Ser	Asp	Ala 130	Lys	Thr	Met	Tyr	Glu 135
Val	Phe	Gln	Arg	Gly 140	Leu	Ala	Val	Ser	Asp 145	Asn	Gly	Pro	Cys	Leu 150
Gly	Tyr	Arg	Lys	Pro 155	Asn	Gln	Pro	Tyr	Arg 160	Trp	Leu	Ser	Tyr	Lys 165
Gln	Val	Ser	Asp	Arg 170	Ala	Glu	Tyr	Leu	Gly 175	Ser	Cys	Leu	Leu	His 180
Lys	Gly	Tyr	Lys	Ser 185	Ser	Pro	Asp	Gln	Phe 190	Val	Gly	Ile	Phe	Ala 195
Gln	Asn	Arg	Pro	Glu 200	Trp	Ile	Ile	Ser	Glu 205	Leu	Ala	Cys	Tyr	Thr 210
Tyr	Ser	Met	Val	Ala 215	Val	Pro	Leu	Tyr	Asp 220	Thr	Leu	Gly	Pro	Glu 225
Ala	Ile	Val	His	Ile 230	Val	Asn	Lys	Ala	Asp 235	Ile	Ala	Met	Val	Ile 240
Cys	Asp	Thr	Pro	Gln 245	Lys	Ala	Leu	Val	Leu 250	Ile	Gly	Asn	Val	Glu 255
Lys	Gly	Phe	Thr	Pro 260	Ser	Leu	Lys	Val	Ile 265	Ile	Leu	Met	Asp	Pro 270
Phe	Asp	Asp	Asp	Leu 275	Lys	Gln	Arg	Gly	Glu 280	Lys	Ser	Gly	Ile	Glu 285
Ile	Leu	Ser	Leu	Tyr 290	Asp	Ala	Glu	Asn	Leu 295	Gly	Lys	Glu	His	Phe 300
Arg	Lys	Pro	Val	Pro 305	Pro	Ser	Pro	Glu	Asp 310	Leu	Ser	Val	Ile	Cys 315
Phe	Thr	Ser	Gly	Thr	Thr	Gly	Asp	Pro	Lys	Gly	Ala	Met	Ile	Thr

320	325	330
His Gln Asn Ile Val Ser Asn Ala Ala	Ala Phe Leu Lys Cys Val	
335	340	345
Glu His Ala Tyr Glu Pro Thr Pro Asp	Asp Val Ala Ile Ser Tyr	
350	355	360
Leu Pro Leu Ala His Met Phe Glu Arg	Ile Val Gln Ala Val Val	
365	370	375
Tyr Ser Cys Gly Ala Arg Val Gly Phe	Phe Gln Gly Asp Ile Arg	
380	385	390
Leu Leu Ala Asp Asp Met Lys Thr Leu	Lys Pro Thr Leu Phe Pro	
395	400	405
Ala Val Pro Arg Leu Leu Asn Arg Ile	Tyr Asp Lys Val Gln Asn	
410	415	420
Glu Ala Lys Thr Pro Leu Lys Lys Phe	Leu Leu Lys Leu Ala Val	
425	430	435
Ser Ser Lys Phe Lys Glu Leu Gln Lys	Gly Ile Ile Arg His Asp	
440	445	450
Ser Phe Trp Asp Lys Leu Ile Phe Ala	Lys Ile Gln Asp Ser Leu	
455	460	465
Gly Gly Arg Val Arg Val Ile Val Thr	Gly Ala Ala Pro Met Ser	
470	475	480
Thr Ser Val Met Thr Phe Phe Arg Ala	Ala Met Gly Cys Gln Val	
485	490	495
Tyr Glu Ala Tyr Gly Gln Thr Glu Cys	Thr Gly Gly Cys Thr Phe	
500	505	510
Thr Leu Pro Gly Asp Trp Thr Ser Gly	His Val Gly Val Pro Leu	
515	520	525
Ala Cys Asn Tyr Val Lys Leu Glu Asp	Val Ala Asp Met Asn Tyr	
530	535	540
Phe Thr Val Asn Asn Glu Gly Glu Val	Cys Ile Lys Gly Thr Asn	
545	550	555
Val Phe Lys Gly Tyr Leu Lys Asp Pro	Glu Lys Thr Gln Glu Ala	
560	565	570
Leu Asp Ser Asp Gly Trp Leu His Thr	Gly Asp Ile Gly Arg Trp	
575	580	585
Leu Pro Asn Gly Thr Leu Lys Ile Ile	Asp Arg Lys Lys Asn Ile	
590	595	600
Phe Lys Leu Ala Gln Gly Glu Tyr Ile	Ala Pro Glu Lys Ile Glu	
605	610	615

Leu	Asn	Gln	Ala	Thr 140	Gly	His	Val	Met	Ala 145	Lys	Arg	Val	Phe	Asp 150
Thr	Tyr	Ser	Pro	His 155	Glu	Asp	Glu	Ala	Met 160	Val	Leu	Phe	Leu	Asn 165
Met	Val	Ala	Pro	Gly 170	Arg	Val	Leu	Ile	Cys 175	Thr	Val	Lys	Asp	Glu 180
Gly	Ser	Phe	His	Leu 185	Lys	Asp	Thr	Ala	Lys 190	Ala	Leu	Leu	Arg	Ser 195
Leu	Gly	Ser	Gln	Ala 200	Gly	Pro	Ala	Leu	Gly 205	Trp	Arg	Asp	Thr	Trp 210
Ala	Phe	Val	Gly	Arg 215	Lys	Gly	Gly	Pro	Val 220	Phe	Gly	Glu	Lys	His 225
Ser	Lys	Ser	Pro	Ala 230	Leu	Ser	Ser	Trp	Gly 235	Asp	Pro	Val	Leu	Leu 240
Lys	Thr	Asp	Val	Pro 245	Leu	Ser	Ser	Ala	Glu 250	Glu	Ala	Glu	Cys	His 255
Trp	Ala	Asp	Thr	Glu 260	Leu	Asn	Arg	Arg	Arg 265	Arg	Arg	Phe	Cys	Ser 270
Lys	Val	Glu	Gly	Tyr 275	Gly	Ser	Val	Cys	Ser 280	Cys	Lys	Asp	Pro	Thr 285
Pro	Ile	Glu	Phe	Ser 290	Pro	Asp	Pro	Leu	Pro 295	Asp	Asn	Lys	Val	Leu 300
Asn	Val	Pro	Val	Ala 305	Val	Ile	Ala	Gly	Asn 310	Arg	Pro	Asn	Tyr	Leu 315
Tyr	Arg	Met	Leu	Arg 320	Ser	Leu	Leu	Ser	Ala 325	Gln	Gly	Val	Ser	Pro 330
Gln	Met	Ile	Thr	Val 335	Phe	Ile	Asp	Gly	Tyr 340	Tyr	Glu	Glu	Pro	Met 345
Asp	Val	Val	Ala	Leu 350	Phe	Gly	Leu	Arg	Gly 355	Ile	Gln	His	Thr	Pro 360
Ile	Ser	Ile	Lys	Asn 365	Ala	Arg	Val	Ser	Gln 370	His	Tyr	Lys	Ala	Ser 375
Leu	Thr	Ala	Thr	Phe 380	Asn	Leu	Phe	Pro	Glu 385	Ala	Lys	Phe	Ala	Val 390
Val	Leu	Glu	Glu	Asp 395	Leu	Asp	Ile	Ala	Val 400	Asp	Phe	Phe	Ser	Phe 405
Leu	Ser	Gln	Ser	Ile 410	His	Leu	Leu	Glu	Glu 415	Asp	Asp	Ser	Leu	Tyr 420
Cys	Ile	Ser	Ala	Trp	Asn	Asp	Gln	Gly	Tyr	Glu	His	Thr	Ala	Glu

425	430	435
Asp Pro Ala Leu Leu Tyr Arg Val Glu	Thr Met Pro Gly Leu Gly	
440	445	450
Trp Val Leu Arg Arg Ser Leu Tyr Lys	Glu Glu Leu Glu Pro Lys	
455	460	465
Trp Pro Thr Pro Glu Lys Leu Trp Asp	Trp Asp Met Trp Met Arg	
470	475	480
Met Pro Glu Gln Arg Arg Gly Arg Glu	Cys Ile Ile Pro Asp Val	
485	490	495
Ser Arg Ser Tyr His Phe Gly Ile Val	Gly Leu Asn Met Asn Gly	
500	505	510
Tyr Phe His Glu Ala Tyr Phe Lys Lys	His Lys Phe Asn Thr Val	
515	520	525
Pro Gly Val Gln Leu Arg Asn Val Asp	Ser Leu Lys Lys Glu Ala	
530	535	540
Tyr Glu Val Glu Val His Arg Leu Leu	Ser Glu Ala Glu Val Leu	
545	550	555
Asp His Ser Lys Asn Pro Cys Glu Asp	Ser Phe Leu Pro Asp Thr	
560	565	570
Glu Gly His Thr Tyr Val Ala Phe Ile	Arg Met Glu Lys Asp Asp	
575	580	585
Asp Phe Thr Thr Trp Thr Gln Leu Ala	Lys Cys Leu His Ile Trp	
590	595	600
Asp Leu Asp Val Arg Gly Asn His Arg	Gly Leu Trp Arg Leu Phe	
605	610	615
Arg Lys Lys Asn His Phe Leu Val Val	Gly Val Pro Ala Ser Pro	
620	625	630
Tyr Ser Val Lys Lys Pro Pro Ser Val	Thr Pro Ile Phe Leu Glu	
635	640	645
Pro Pro Pro Lys Glu Glu Gly Ala Pro	Gly Ala Pro Glu Gln Thr	
650	655	660

<210> 89

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 89

<400> 94

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actggaaatt tggtgtctag tgggtgtggg tgaataaagg agggcagaat 150
ggatgatttc atctccatta gcctgctgtc tctggctatg ttggtgggat 200
gttacgtggc cggaatcatt cccttggtg ttaatttctc agaggaacga 250
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aaaaggccct tgacattttg cgttttaata tttctcttaa ccctattctc 1350
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<212> DNA
<213> Homo sapiens

<400> 99

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Ile Leu Glu His	Leu Tyr Pro Thr Met	Asp Ser Gly Glu Trp	Asp
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Val Leu Ile Ala	His Phe Leu Gly Val	Asp His Cys Gly His	Lys
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His Gly Pro His	His Pro Glu Met Ala	Lys Lys Leu Ser Gln	Met
	245	250	255
Asp Gln Val Ile	Gln Gly Leu Val Glu	Arg Leu Glu Asn Asp	Thr
	260	265	270
Leu Leu Val Val	Ala Gly Asp His Gly	Met Thr Thr Asn Gly	Asp
	275	280	285
His Gly Gly Asp	Ser Glu Leu Glu Val	Ser Ala Ala Leu Phe	Leu
	290	295	300
Tyr Ser Pro Thr	Ala Val Phe Pro Ser	Thr Pro Pro Glu Glu	Pro
	305	310	315
Glu Val Ile Pro	Gln Val Ser Leu Val	Pro Thr Leu Ala Leu	Leu
	320	325	330
Leu Gly Leu Pro	Ile Pro Phe Gly Asn	Ile Gly Glu Val Met	Ala
	335	340	345
Glu Leu Phe Ser	Gly Gly Glu Asp Ser	Gln Pro His Ser Ser	Ala
	350	355	360
Leu Ala Gln Ala	Ser Ala Leu His Leu	Asn Ala Gln Gln Val	Ser
	365	370	375
Arg Phe Leu His	Thr Tyr Ser Ala Ala	Thr Gln Asp Leu Gln	Ala
	380	385	390
Lys Glu Leu His	Gln Leu Gln Asn Leu	Phe Ser Lys Ala Ser	Ala
	395	400	405
Asp Tyr Gln Trp	Leu Leu Gln Ser Pro	Lys Gly Ala Glu Ala	Thr
	410	415	420
Leu Pro Thr Val	Ile Ala Glu Leu Gln	Gln Phe Leu Arg Gly	Ala
	425	430	435
Arg Ala Met Cys	Ile Glu Ser Trp Ala	Arg Phe Ser Leu Val	Arg
	440	445	450
Met Ala Gly Gly	Thr Ala Leu Leu Ala	Ala Ser Cys Phe Ile	Cys
	455	460	465
Leu Leu Ala Ser	Gln Trp Ala Ile Ser	Pro Gly Phe Pro Phe	Cys
	470	475	480
Pro Leu Leu Leu	Thr Pro Val Ala Trp	Gly Leu Val Gly Ala	Ile
	485	490	495

Ala Tyr Ala Gly	Leu Leu Gly Thr Ile	Glu Leu Lys Leu Asp	Leu
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Val Leu Leu Gly	Ala Val Ala Ala Val	Ser Ser Phe Leu Pro	Phe
515		520	525
Leu Trp Lys Ala	Trp Ala Gly Trp Gly	Ser Lys Arg Pro Leu	Ala
530		535	540
Thr Leu Phe Pro	Ile Pro Gly Pro Val	Leu Leu Leu Leu Leu	Phe
545		550	555
Arg Leu Ala Val	Phe Phe Ser Asp Ser	Phe Val Val Ala Glu	Ala
560		565	570
Arg Ala Thr Pro	Phe Leu Leu Gly Ser	Phe Ile Leu Leu Leu	Val
575		580	585
Val Gln Leu His	Trp Glu Gly Gln Leu	Leu Pro Pro Lys Leu	Leu
590		595	600
Thr Met Pro Arg	Leu Gly Thr Ser Ala	Thr Thr Asn Pro Pro	Arg
605		610	615
His Asn Gly Ala	Tyr Ala Leu Arg Leu	Gly Ile Gly Leu Leu	Leu
620		625	630
Cys Thr Arg Leu	Ala Gly Leu Phe His	Arg Cys Pro Glu Glu	Thr
635		640	645
Pro Val Cys His	Ser Ser Pro Trp Leu	Ser Pro Leu Ala Ser	Met
650		655	660
Val Gly Gly Arg	Ala Lys Asn Leu Trp	Tyr Gly Ala Cys Val	Ala
665		670	675
Ala Leu Val Ala	Leu Leu Ala Ala Val	Arg Leu Trp Leu Arg	Arg
680		685	690
Tyr Gly Asn Leu	Lys Ser Pro Glu Pro	Pro Met Leu Phe Val	Arg
695		700	705
Trp Gly Leu Pro	Leu Met Ala Leu Gly	Thr Ala Ala Tyr Trp	Ala
710		715	720
Leu Ala Ser Gly	Ala Asp Glu Ala Pro	Pro Arg Leu Arg Val	Leu
725		730	735
Val Ser Gly Ala	Ser Met Val Leu Pro	Arg Ala Val Ala Gly	Leu
740		745	750
Ala Ala Ser Gly	Leu Ala Leu Leu Leu	Trp Lys Pro Val Thr	Val
755		760	765
Leu Val Lys Ala	Gly Ala Gly Ala Pro	Arg Thr Arg Thr Val	Leu
770		775	780
Thr Pro Phe Ser	Gly Pro Pro Thr Ser	Gln Ala Asp Leu Asp	Tyr

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Val	Val	Pro	Gln	Ile 800	Tyr	Arg	His	Met	Gln 805	Glu	Glu	Phe	Arg	Gly 810
Arg	Leu	Glu	Arg	Thr 815	Lys	Ser	Gln	Gly	Pro 820	Leu	Thr	Val	Ala	Ala 825
Tyr	Gln	Leu	Gly	Ser 830	Val	Tyr	Ser	Ala	Ala 835	Met	Val	Thr	Ala	Leu 840
Thr	Leu	Leu	Ala	Phe 845	Pro	Leu	Leu	Leu	Leu 850	His	Ala	Glu	Arg	Ile 855
Ser	Leu	Val	Phe	Leu 860	Leu	Leu	Phe	Leu	Gln 865	Ser	Phe	Leu	Leu	Leu 870
His	Leu	Leu	Ala	Ala 875	Gly	Ile	Pro	Val	Thr 880	Thr	Pro	Gly	Pro	Phe 885
Thr	Val	Pro	Trp	Gln 890	Ala	Val	Ser	Ala	Trp 895	Ala	Leu	Met	Ala	Thr 900
Gln	Thr	Phe	Tyr	Ser 905	Thr	Gly	His	Gln	Pro 910	Val	Phe	Pro	Ala	Ile 915
His	Trp	His	Ala	Ala 920	Phe	Val	Gly	Phe	Pro 925	Glu	Gly	His	Gly	Ser 930
Cys	Thr	Trp	Leu	Pro 935	Ala	Leu	Leu	Val	Gly 940	Ala	Asn	Thr	Phe	Ala 945
Ser	His	Leu	Leu	Phe 950	Ala	Val	Gly	Cys	Pro 955	Leu	Leu	Leu	Leu	Trp 960
Pro	Phe	Leu	Cys	Glu 965	Ser	Gln	Gly	Leu	Arg 970	Lys	Arg	Gln	Gln	Pro 975
Pro	Gly	Asn	Glu	Ala 980	Asp	Ala	Arg	Val	Arg 985	Pro	Glu	Glu	Glu	Glu 990
Glu	Pro	Leu	Met	Glu 995	Met	Arg	Leu	Arg	Asp 1000	Ala	Pro	Gln	His	Phe 1005
Tyr	Ala	Ala	Leu	Leu 1010	Gln	Leu	Gly	Leu	Lys 1015	Tyr	Leu	Phe	Ile	Leu 1020
Gly	Ile	Gln	Ile	Leu 1025	Ala	Cys	Ala	Leu	Ala 1030	Ala	Ser	Ile	Leu	Arg 1035
Arg	His	Leu	Met	Val 1040	Trp	Lys	Val	Phe	Ala 1045	Pro	Lys	Phe	Ile	Phe 1050
Glu	Ala	Val	Gly	Phe 1055	Ile	Val	Ser	Ser	Val 1060	Gly	Leu	Leu	Leu	Gly 1065
Ile	Ala	Leu	Val	Met 1070	Arg	Val	Asp	Gly	Ala 1075	Val	Ser	Ser	Trp	Phe 1080

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1085

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<211> 1743
<212> DNA
<213> Homo sapiens

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cttatccatc aacatgaaga atgtcctaca atggaactcca ccagagggtc 150
ttcaaggagt taaagttact tacactgtgc agtatttcat cacaaattgg 200
cccaccagag gtggcactga ctacagatga gaagtccatt tctgttgtcc 250
tgacagctcc agagaagtgg aagagaaatc cagaagacct tctgttttcc 300
atgcaacaaa tatactccaa tctgaagtat aacgtgtctg tgttgaatac 350
taaatacaac agaacgtggt ccagtggtg gaccaaccac acgctgggtgc 400
tcacctggct ggagccgaac actctttact gcgtacacgt ggagtccttc 450
gtcccagggc cccctcgccg tgctcagcct tctgagaagc agtgtgccag 500
gactttgaaa gatcaatcat cagagttcaa ggctaaaatc atcttctggt 550
atgttttgcc catatctatt accgtgtttc ttttttctgt gatgggctat 600
tccatctacc gatatatcca cgttggcaaa gagaaacacc cagcaaattt 650
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Tyr	Gly	Asn	Glu	Phe 185	Asp	Lys	Arg	Phe	Phe 190	Val	Pro	Ala	Glu	Lys 195
Ile	Val	Ile	Asn	Phe 200	Ile	Thr	Leu	Asn	Ile 205	Ser	Asp	Asp	Ser	Lys 210
Ile	Ser	His	Gln	Asp 215	Met	Ser	Leu	Leu	Gly 220	Lys	Ser	Ser	Asp	Val 225
Ser	Ser	Leu	Asn	Asp 230	Pro	Gln	Pro	Ser	Gly 235	Asn	Leu	Arg	Pro	Pro 240
Gln	Glu	Glu	Glu	Glu 245	Val	Lys	His	Leu	Gly 250	Tyr	Ala	Ser	His	Leu 255
Met	Glu	Ile	Phe	Cys 260	Asp	Ser	Glu	Glu	Asn 265	Thr	Glu	Gly	Thr	Ser 270
Leu	Thr	Gln	Gln	Glu 275	Ser	Leu	Ser	Arg	Thr 280	Ile	Pro	Pro	Asp	Lys 285
Thr	Val	Ile	Glu	Tyr 290	Glu	Tyr	Asp	Val	Arg 295	Thr	Thr	Asp	Ile	Cys 300
Ala	Gly	Pro	Glu	Glu 305	Gln	Glu	Leu	Ser	Leu 310	Gln	Glu	Glu	Val	Ser 315
Thr	Gln	Gly	Thr	Leu 320	Leu	Glu	Ser	Gln	Ala 325	Ala	Leu	Ala	Val	Leu 330
Gly	Pro	Gln	Thr	Leu 335	Gln	Tyr	Ser	Tyr	Thr 340	Pro	Gln	Leu	Gln	Asp 345
Leu	Asp	Pro	Leu	Ala 350	Gln	Glu	His	Thr	Asp 355	Ser	Glu	Glu	Gly	Pro 360
Glu	Glu	Glu	Pro	Ser 365	Thr	Thr	Leu	Val	Asp 370	Trp	Asp	Pro	Gln	Thr 375
Gly	Arg	Leu	Cys	Ile 380	Pro	Ser	Leu	Ser	Ser 385	Phe	Asp	Gln	Asp	Ser 390
Glu	Gly	Cys	Glu	Pro 395	Ser	Glu	Gly	Asp	Gly 400	Leu	Gly	Glu	Glu	Gly 405
Leu	Leu	Ser	Arg	Leu 410	Tyr	Glu	Glu	Pro	Ala 415	Pro	Asp	Arg	Pro	Pro 420
Gly	Glu	Asn	Glu	Thr 425	Tyr	Leu	Met	Gln	Phe 430	Met	Glu	Glu	Trp	Gly 435
Leu	Tyr	Val	Gln	Met 440	Glu	Asn								

118

<211> 21
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 <213> Artificial

 <220>
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 <222> 1-21
 <223> Synthetic construct

 <400> 105
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 <210> 106
 <211> 18
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

 <400> 106
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 <210> 107
 <211> 18
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

 <400> 107
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 <210> 108
 <211> 25
 <212> DNA
 <213> Artificial

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 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

 <400> 108
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 <210> 109
 <211> 51
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence

<222> 1-51
<223> Synthetic construct.

<400> 109
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c 51

<210> 110
<211> 1114
<212> DNA
<213> Homo sapiens

<400> 110
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<210> 111

<211> 283

<212> PRT

<213> Homo sapiens

<400> 111

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				20					25					30
Gly	Ala	Gln	Ile	Ile	Gly	Gly	His	Glu	Val	Thr	Pro	His	Ser	Arg
			35						40					45
Pro	Tyr	Met	Ala	Ser	Val	Arg	Phe	Gly	Gly	Gln	His	His	Cys	Gly
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Gly	Phe	Leu	Leu	Arg	Ala	Arg	Trp	Val	Val	Ser	Ala	Ala	His	Cys
				65					70					75
Phe	Ser	His	Arg	Asp	Leu	Arg	Thr	Gly	Leu	Val	Val	Leu	Gly	Ala
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His	Val	Leu	Ser	Thr	Ala	Glu	Pro	Thr	Gln	Gln	Val	Phe	Gly	Ile
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Asp	Ala	Leu	Thr	Thr	His	Pro	Asp	Tyr	His	Pro	Met	Thr	His	Ala
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Asn	Asp	Ile	Cys	Leu	Leu	Arg	Leu	Asn	Gly	Ser	Ala	Val	Leu	Gly
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Pro	Ala	Val	Gly	Leu	Leu	Arg	Leu	Pro	Gly	Arg	Arg	Ala	Arg	Pro
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Pro	Thr	Ala	Gly	Thr	Arg	Cys	Arg	Val	Ala	Gly	Trp	Gly	Phe	Val
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Ser	Asp	Phe	Glu	Glu	Leu	Pro	Pro	Gly	Leu	Met	Glu	Ala	Lys	Val
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Arg	Val	Leu	Asp	Pro	Asp	Val	Cys	Asn	Ser	Ser	Trp	Lys	Gly	His
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Leu	Thr	Leu	Thr	Met	Leu	Cys	Thr	Arg	Ser	Gly	Asp	Ser	His	Arg
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Arg	Gly	Phe	Cys	Ser	Ala	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Arg
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Asn	Arg	Ala	His	Gly	Leu	Val	Ser	Phe	Ser	Gly	Leu	Trp	Cys	Gly
				230					235					240
Asp	Pro	Lys	Thr	Pro	Asp	Val	Tyr	Thr	Gln	Val	Ser	Ala	Phe	Val
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<210> 116
 <211> 331
 <212> PRT
 <213> Homo sapiens

<400> 116

Met	Ser	Arg	Tyr	Leu	Leu	Pro	Leu	Ser	Ala	Leu	Gly	Thr	Val	Ala	
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Gly	Ala	Ala	Val	Leu	Leu	Lys	Asp	Tyr	Val	Thr	Gly	Gly	Ala	Cys	
				20					25					30	
Pro	Ser	Lys	Ala	Thr	Ile	Pro	Gly	Lys	Thr	Val	Ile	Val	Thr	Gly	
				35					40					45	
Ala	Asn	Thr	Gly	Ile	Gly	Lys	Gln	Thr	Ala	Leu	Glu	Leu	Ala	Arg	
				50					55					60	
Arg	Gly	Gly	Asn	Ile	Ile	Leu	Ala	Cys	Arg	Asp	Met	Glu	Lys	Cys	
				65					70					75	
Glu	Ala	Ala	Ala	Lys	Asp	Ile	Arg	Gly	Glu	Thr	Leu	Asn	His	His	
				80					85					90	
Val	Asn	Ala	Arg	His	Leu	Asp	Leu	Ala	Ser	Leu	Lys	Ser	Ile	Arg	
				95					100					105	
Glu	Phe	Ala	Ala	Lys	Ile	Ile	Glu	Glu	Glu	Glu	Arg	Val	Asp	Ile	
				110					115					120	
Leu	Ile	Asn	Asn	Ala	Gly	Val	Met	Arg	Cys	Pro	His	Trp	Thr	Thr	
				125					130					135	
Glu	Asp	Gly	Phe	Glu	Met	Gln	Phe	Gly	Val	Asn	His	Leu	Gly	His	
				140					145					150	
Phe	Leu	Leu	Thr	Asn	Leu	Leu	Leu	Asp	Lys	Leu	Lys	Ala	Ser	Ala	
				155					160					165	
Pro	Ser	Arg	Ile	Ile	Asn	Leu	Ser	Ser	Leu	Ala	His	Val	Ala	Gly	
				170					175					180	
His	Ile	Asp	Phe	Asp	Asp	Leu	Asn	Trp	Gln	Thr	Arg	Lys	Tyr	Asn	
				185					190					195	
Thr	Lys	Ala	Ala	Tyr	Cys	Gln	Ser	Lys	Leu	Ala	Ile	Val	Leu	Phe	
				200					205					210	
Thr	Lys	Glu	Leu	Ser	Arg	Arg	Leu	Gln	Gly	Ser	Gly	Val	Thr	Val	
				215					220					225	

TCAGGCTCTGCA

Ser Pro Glu Asp

<210> 119
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 119
cgggacagga gacccagaaa ggg 23

<210> 120
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 120
ggccaagtga tccaaggcat cttc 24

<210> 121
<211> 49
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-49
<223> Synthetic construct.

<400> 121
ctgcgggacc tgactagatt ctacgacaag gtactttctt tgcattggg 49

<210> 122
<211> 1778
<212> DNA
<213> Homo sapiens

<400> 122
gagatagggga gtctgggttt aagttcctgc tccatctcag gagcccctgc 50
tccccccct aggaagccac cagactccac ggtgtggggc caatcagggtg 100
gaatcggccc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150
ggagagcccc ggagcccccg taaccgcgc ggggagcgcc caggatgccg 200

cgcggggact cggagcaggt gcgctactgc gcgcgcttct cctacctctg 250
 gctcaagttt tcacttatca tctattccac cgtgttcttg ctgattgggg 300
 ccctggtcct gtctgtgggc atctatgcag aggttgagcg gcagaaatat 350
 aaaacccttg aaagtgcctt cctggctcca gccatcatcc tcatcctcct 400
 gggcgctcgtc atgttcatgg tctccttcat tgggtgtgctg gcgtccctcc 450
 gtgacaacct gtaccttctc caagcattca tgtacatcct tgggatctgc 500
 ctcatcatgg agctcattgg tggcgtgggtg gccttgacct tccggaacca 550
 gaccattgac ttctgaacg acaacattcg aagaggaatt gagaactact 600
 atgatgatct ggacttcaaa aacatcatgg actttgttca gaaaaagttc 650
 aagtgtctgtg gcggggagga ctaccgagat tggagcaaga atcagtacca 700
 cgactgcagt gccctggac ccctggcctg tggggtgccc tacacctgct 750
 gcatcaggaa cagcacagaa gttgtcaaca ccatgtgtgg ctacaaaact 800
 atcgacaagg agcgtttcag tgtgcaggat gtcattctacg tgcggggctg 850
 caccaacgcc gtgatcatct ggttcatgga caactacacc atcatggcgt 900
 gcatcctcct gggcatcctg cttccccagt tctgggggt gctgctgacg 950
 ctgctgtaca tcaccgggt ggaggacatc atcatggagc actctgtcac 1000
 tgatgggctc ctggggcccgt gtgccaagcc cagcgtggag gcggcaggca 1050
 cgggatgctg cttgtgctac cccaattagg gccagcctg ccatggcagc 1100
 tccaacaagg accgtctggg atagcacctc tcagtcaaca tcgtggggct 1150
 ggacagggct gcggcccctc tgcccacact cagtactgac caaagccagg 1200
 gctgtgtgtg cctgtgtgta ggtccacagg cctctgcctc ccaggaggc 1250
 agagcctggg cctcccctaa gaggctttcc ccgaggcagc tctggaatct 1300
 gtgccacct ggggcctggg gaacaaggcc ctcccttctc caggcctggg 1350
 ctacagggga gggagagcct gaggtctctg tcaggggcca tttcatctct 1400
 ggcatgtcct tggcgtgtgt attcaaggca gttttgtagc acctgtaatt 1450
 ggggagaggg agtgtgcccc tcggggcagg agggaagggc atctggggaa 1500
 gggcaggagg gaagagctgt ccatgcagcc acgcccattg ccaggttggc 1550
 ctcttctcag cctcccagggt gccttgagcc ctcttgcaag ggcggtgct 1600
 tccttgagcc tagttttttt ttacgtgatt tttgtaacat tcattttttt 1650

gtacagataa caggagtttc tgactaatca aagctggtat ttccccgcat 1700
 gtcttattct tgcccttccc ccaaccagtt tgттаатcaa асаатааааа 1750
 catgttttgt tttgttttta аааааааа 1778

<210> 123
 <211> 294
 <212> PRT
 <213> Homo sapiens

<400> 123
 Met Pro Arg Gly Asp Ser Glu Gln Val Arg Tyr Cys Ala Arg Phe
 1 5 10 15
 Ser Tyr Leu Trp Leu Lys Phe Ser Leu Ile Ile Tyr Ser Thr Val
 20 25 30
 Phe Trp Leu Ile Gly Ala Leu Val Leu Ser Val Gly Ile Tyr Ala
 35 40 45
 Glu Val Glu Arg Gln Lys Tyr Lys Thr Leu Glu Ser Ala Phe Leu
 50 55 60
 Ala Pro Ala Ile Ile Leu Ile Leu Leu Gly Val Val Met Phe Met
 65 70 75
 Val Ser Phe Ile Gly Val Leu Ala Ser Leu Arg Asp Asn Leu Tyr
 80 85 90
 Leu Leu Gln Ala Phe Met Tyr Ile Leu Gly Ile Cys Leu Ile Met
 95 100 105
 Glu Leu Ile Gly Gly Val Val Ala Leu Thr Phe Arg Asn Gln Thr
 110 115 120
 Ile Asp Phe Leu Asn Asp Asn Ile Arg Arg Gly Ile Glu Asn Tyr
 125 130 135
 Tyr Asp Asp Leu Asp Phe Lys Asn Ile Met Asp Phe Val Gln Lys
 140 145 150
 Lys Phe Lys Cys Cys Gly Gly Glu Asp Tyr Arg Asp Trp Ser Lys
 155 160 165
 Asn Gln Tyr His Asp Cys Ser Ala Pro Gly Pro Leu Ala Cys Gly
 170 175 180
 Val Pro Tyr Thr Cys Cys Ile Arg Asn Thr Thr Glu Val Val Asn
 185 190 195
 Thr Met Cys Gly Tyr Lys Thr Ile Asp Lys Glu Arg Phe Ser Val
 200 205 210
 Gln Asp Val Ile Tyr Val Arg Gly Cys Thr Asn Ala Val Ile Ile
 215 220 225
 Trp Phe Met Asp Asn Tyr Thr Ile Met Ala Cys Ile Leu Leu Gly

Ser Ile Asp Arg	Leu Glu Phe Asp Leu	Leu Tyr Pro Ala Ile	Lys
230	235		240
Gly Asp Thr Ile	Gln Leu Tyr Leu Gly	Ala Lys Leu Leu Asp	Ser
245	250		255
Gln Gly Lys Val	Thr Lys Trp Phe Asn	Asn Ser Ala Ala Ser	Leu
260	265		270
Thr Met Pro Thr	Leu Asp Asn Ile Pro	Phe Ser Leu Ile Val	Ser
275	280		285
Gln Asp Val Val	Lys Ala Ala Val Ala	Ala Val Leu Ser Pro	Glu
290	295		300
Glu Phe Met Val	Leu Leu Asp Ser Val	Leu Pro Glu Ser Ala	His
305	310		315
Arg Leu Lys Ser	Ser Ile Gly Leu Ile	Asn Glu Lys Ala Ala	Asp
320	325		330
Lys Leu Gly Ser	Thr Gln Ile Val Lys	Ile Leu Thr Gln Asp	Thr
335	340		345
Pro Glu Phe Phe	Ile Asp Gln Gly His	Ala Lys Val Ala Gln	Leu
350	355		360
Ile Val Leu Glu	Val Phe Pro Ser Ser	Glu Ala Leu Arg Pro	Leu
365	370		375
Phe Thr Leu Gly	Ile Glu Ala Ser Ser	Glu Ala Gln Phe Tyr	Thr
380	385		390
Lys Gly Asp Gln	Leu Ile Leu Asn Leu	Asn Asn Ile Ser Ser	Asp
395	400		405
Arg Ile Gln Leu	Met Asn Ser Gly Ile	Gly Trp Phe Gln Pro	Asp
410	415		420
Val Leu Lys Asn	Ile Ile Thr Glu Ile	Ile His Ser Ile Leu	Leu
425	430		435
Pro Asn Gln Asn	Gly Lys Leu Arg Ser	Gly Val Pro Val Ser	Leu
440	445		450
Val Lys Ala Leu	Gly Phe Glu Ala Ala	Glu Ser Ser Leu Thr	Lys
455	460		465
Asp Ala Leu Val	Leu Thr Pro Ala Ser	Leu Trp Lys Pro Ser	Ser
470	475		480
Pro Val Ser Gln			

<210> 129
 <211> 2213
 <212> DNA
 <213> Homo sapiens

cttctgtcca ccagtataat aaagagcagt ttatcaagtg gaaacaaagt 1600
 ataggacaga attattcaaa cggtatagca aatcttaggt ggcaccaaga 1650
 ctggcagaag gaaccaagga agtatgaaaa tgcaattgat cagtggctta 1700
 aaacccatat gaatccaaga gcagtttgaa caaaaagttt aaaaatagtg 1750
 ttctagagat acatataaat atattacaag atcataatta tgtattttta 1800
 atgaaacagt ttttaataatt accaagtttt ggccggggcac agtggctcac 1850
 acctgtaatc ccaggacttt gggaggctga ggaaagcaga tcacaaggctc 1900
 aagagattga gaccatcctg gccaacatgg tgaaaccctg tctctactaa 1950
 aaatacaaaa attagctggg cgcggtggtg cacacctata gtctcagcta 2000
 ctcagaggct gaggcaggag gatcgcttga acccgggagg cagcagttgc 2050
 agtgagctga gattgcgcca ctgtactcca gcctggcaac agagtgagac 2100
 tgtgtcgcaa aaaaataaaa ataaaataat aataattacc aatttttcat 2150
 tattttgtaa gaatgtagtg tattttaaga taaaatgcca atgattataa 2200
 aatcacatat tttcaaaaat gggtattatt taggcctttg tacaatttct 2250
 aacaatttag tggaagtatc aaaaggattg aagcaaatac tgtaacagtt 2300
 atgttccttt aaataataga gaatataaaa tattgtaata atatgtatca 2350
 taaaatagtt gtatgtgagc atttgatggt gaaaaaaaaa aaaaaaaaaa 2400
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2450
 aaaaaaaaaa aaaaaaaaaa aaaaaa 2476

<210> 132
 <211> 536
 <212> PRT
 <213> Homo sapiens

<400> 132
 Met Leu Leu Leu Trp Val Ser Val Val Ala Ala Leu Ala Leu Ala
 1 5 10 15
 Val Leu Ala Pro Gly Ala Gly Glu Gln Arg Arg Arg Ala Ala Lys
 20 25 30
 Ala Pro Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg
 35 40 45
 Leu Thr Phe His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile
 50 55 60
 Asn Phe Met Lys Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr
 65 70 75

Asn	Ser	Pro	Ile	Cys	Cys	Pro	Ser	Arg	Ala	Ala	Met	Trp	Ser	Gly	
				80					85					90	
Leu	Phe	Thr	His	Leu	Thr	Glu	Ser	Trp	Asn	Asn	Phe	Lys	Gly	Leu	
				95					100					105	
Asp	Pro	Asn	Tyr	Thr	Thr	Trp	Met	Asp	Val	Met	Glu	Arg	His	Gly	
				110					115					120	
Tyr	Arg	Thr	Gln	Lys	Phe	Gly	Lys	Leu	Asp	Tyr	Thr	Ser	Gly	His	
				125					130					135	
His	Ser	Ile	Ser	Asn	Arg	Val	Glu	Ala	Trp	Thr	Arg	Asp	Val	Ala	
				140					145					150	
Phe	Leu	Leu	Arg	Gln	Glu	Gly	Arg	Pro	Met	Val	Asn	Leu	Ile	Arg	
				155					160					165	
Asn	Arg	Thr	Lys	Val	Arg	Val	Met	Glu	Arg	Asp	Trp	Gln	Asn	Thr	
				170					175					180	
Asp	Lys	Ala	Val	Asn	Trp	Leu	Arg	Lys	Glu	Ala	Ile	Asn	Tyr	Thr	
				185					190					195	
Glu	Pro	Phe	Val	Ile	Tyr	Leu	Gly	Leu	Asn	Leu	Pro	His	Pro	Tyr	
				200					205					210	
Pro	Ser	Pro	Ser	Ser	Gly	Glu	Asn	Phe	Gly	Ser	Ser	Thr	Phe	His	
				215					220					225	
Thr	Ser	Leu	Tyr	Trp	Leu	Glu	Lys	Val	Ser	His	Asp	Ala	Ile	Lys	
				230					235					240	
Ile	Pro	Lys	Trp	Ser	Pro	Leu	Ser	Glu	Met	His	Pro	Val	Asp	Tyr	
				245					250					255	
Tyr	Ser	Ser	Tyr	Thr	Lys	Asn	Cys	Thr	Gly	Arg	Phe	Thr	Lys	Lys	
				260					265					270	
Glu	Ile	Lys	Asn	Ile	Arg	Ala	Phe	Tyr	Tyr	Ala	Met	Cys	Ala	Glu	
				275					280					285	
Thr	Asp	Ala	Met	Leu	Gly	Glu	Ile	Ile	Leu	Ala	Leu	His	Gln	Leu	
				290					295					300	
Asp	Leu	Leu	Gln	Lys	Thr	Ile	Val	Ile	Tyr	Ser	Ser	Asp	His	Gly	
				305					310					315	
Glu	Leu	Ala	Met	Glu	His	Arg	Gln	Phe	Tyr	Lys	Met	Ser	Met	Tyr	
				320					325					330	
Glu	Ala	Ser	Ala	His	Val	Pro	Leu	Leu	Met	Met	Gly	Pro	Gly	Ile	
				335					340					345	
Lys	Ala	Gly	Leu	Gln	Val	Ser	Asn	Val	Val	Ser	Leu	Val	Asp	Ile	
				350					355					360	
Tyr	Pro	Thr	Met	Leu	Asp	Ile	Ala	Gly	Ile	Pro	Leu	Pro	Gln	Asn	

	365		370		375
Leu Ser Gly Tyr	Ser Leu Leu Pro Leu	Ser Ser Glu Thr Phe	Lys		
	380	385	390		
Asn Glu His Lys	Val Lys Asn Leu His	Pro Pro Trp Ile Leu	Ser		
	395	400	405		
Glu Phe His Gly	Cys Asn Val Asn Ala	Ser Thr Tyr Met Leu	Arg		
	410	415	420		
Thr Asn His Trp	Lys Tyr Ile Ala Tyr	Ser Asp Gly Ala Ser	Ile		
	425	430	435		
Leu Pro Gln Leu	Phe Asp Leu Ser Ser	Asp Pro Asp Glu Leu	Thr		
	440	445	450		
Asn Val Ala Val	Lys Phe Pro Glu Ile	Thr Tyr Ser Leu Asp	Gln		
	455	460	465		
Lys Leu His Ser	Ile Ile Asn Tyr Pro	Lys Val Ser Ala Ser	Val		
	470	475	480		
His Gln Tyr Asn	Lys Glu Gln Phe Ile	Lys Trp Lys Gln Ser	Ile		
	485	490	495		
Gly Gln Asn Tyr	Ser Asn Val Ile Ala	Asn Leu Arg Trp His	Gln		
	500	505	510		
Asp Trp Gln Lys	Glu Pro Arg Lys Tyr	Glu Asn Ala Ile Asp	Gln		
	515	520	525		
Trp Leu Lys Thr	His Met Asn Pro Arg	Ala Val			
	530	535			

<210> 133

<211> 1475

<212> DNA

<213> Homo sapiens

<400> 133

gagagaagtc agcctggcag agagactctg aaatgagggg ttagaggtgt 50

tcaaggagca agagcttcag cctgaagaca agggagcagt ccctgaagac 100

gcttctactg agaggtctgc catggcctct cttggcctcc aacttgtggg 150

ctacatccta ggcttcttgg ggcttttggg cacactgggt gccatgctgc 200

tccccagctg gaaaacaagt tcttatgtcg gtgocagcat tgtgacagca 250

gttggtcttct ccaagggcct ctggatggaa tgtgccacac acagcacagg 300

catcaccag tgtgacatct atagcaccct tctgggcctg cccgctgaca 350

tccaggctgc ccaggccatg atggtgacat ccagtgaat ctctccctg 400

gcctgcatta tctctgtggt gggcatgaga tgcacagtct tctgccagga 450

[illegible]

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<210> 135
<211> 610
<212> DNA
<213> Homo sapiens
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<400> 135
gcactgctgc tgtcccatca gctgctctga agtcccatgg tgccagaat 50
cttcgctcct gcttatgtgt cagtctgtct cctcctcttg tgtccaagg 100
aagtcacgc tcccgctggc tcagaacat ggctgtgcca gccggcacc 150
agggtggag acaagatcta caacccttg gagcagtgt gttacaatga 200
cgccatcgtg tccctgagcg agaccgcga atgtggtccc cctgcacct 250
tctggccctg ctttgagctc tgctgtcttg attcctttgg cctcacaac 300
gattttgttg tgaagctgaa ggttcagggt gtgaattccc agtgccactc 350
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gagacc	caga	acccagctct	gccctgtgta	gagtttgatg	agaaggtgac	450
tggaggccct	gggaccaaag	gcaaggggaag	aaggaatgag	aagtacgata		500
tggtgacaga	ctgtggctac	acaatctctc	aagtgagatc	aatgaagatt		550
ctgaagcgat	ttggtggccc	agctggtcta	tggaccaagg	atccactggg		600
gcaaacagag	aagatctacg	tgttagatgg	gacacagaat	gacacagcct		650
ttgtcttccc	aaggctgcgt	gacttcaccc	ttgccatggc	tgcccggaaa		700
gcttcccag	tccgggtgcc	cttcccctgg	gtaggcacag	ggcagctggt		750
atatggtggc	tttctttatt	ttgctcggag	gcctcctgga	agacctggtg		800
gaggtggtga	gatggagaac	actttgcagc	taatcaaatt	ccacctggca		850
aaccgaacag	tggtggacag	ctcagtattc	ccagcagagg	ggctgatccc		900
cccctacggc	ttgacagcag	acacctacat	cgacctggta	gctgatgagg		950
aaggtctttg	ggctgtctat	gccacccggg	aggatgacag	gcacttgtgt		1000
ctggccaagt	tagatccaca	gacactggac	acagagcagc	agtgggacac		1050
accatgtccc	agagagaatg	ctgaggctgc	ctttgtcatc	tgtgggaccc		1100
tctatgtcgt	ctataacacc	cgtcctgcca	gtcgggcccg	catccagtgc		1150
tcctttgatg	ccagcggcac	cctgaccct	gaacgggcag	cactccctta		1200
ttttccccgc	agatatggtg	cccatgccag	cctccgctat	aacccccgag		1250
aacgccagct	ctatgcctgg	gatgatggct	accagattgt	ctataagctg		1300
gagatgagga	agaaagagga	ggaggtttga	ggagctagcc	ttgttttttg		1350
catctttctc	actcccatac	atttatatta	tatccccact	aaatttcttg		1400
ttcctcattc	ttcaaagtgt	ggccagttgt	ggctcaaatc	ctctatatatt		1450
ttagccaatg	gcaatcaaat	tctttcagct	cctttgtttc	atacggaact		1500
ccagatcctg	agtaatcctt	ttagagcccg	aagagtcaaa	accctcaatg		1550
ttccctcctg	ctctcctgcc	ccatgtcaac	aaatttcagg	ctaaggatgc		1600
cccagaccca	gggctctaac	cttgtagtgcg	ggcaggccca	gggagcaggc		1650
agcagtgttc	ttcccctcag	agtgacttgg	ggagggagaa	ataggaggag		1700
acgtccagct	ctgtcctctc	ttcctcactc	ctcccttcag	tgtcctgagg		1750
aacaggactt	tctccacatt	gttttgtatt	gcaacatttt	gcattaaaag		1800
gaaaatccac	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa		1850

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1883

<210> 146

<211> 406

<212> PRT

<213> Homo sapiens

<400> 146

Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp
1 5 10 15

Ser Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met
20 25 30

Glu Arg Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln
35 40 45

Asp Gln Ser Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn
50 55 60

Lys Met Leu Pro Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Ala
65 70 75

Leu Arg Thr Glu Ala Asp Thr Ile Ser Gly Arg Val Asp Arg Leu
80 85 90

Glu Arg Glu Val Asp Tyr Leu Glu Thr Gln Asn Pro Ala Leu Pro
95 100 105

Cys Val Glu Phe Asp Glu Lys Val Thr Gly Gly Pro Gly Thr Lys
110 115 120

Gly Lys Gly Arg Arg Asn Glu Lys Tyr Asp Met Val Thr Asp Cys
125 130 135

Gly Tyr Thr Ile Ser Gln Val Arg Ser Met Lys Ile Leu Lys Arg
140 145 150

Phe Gly Gly Pro Ala Gly Leu Trp Thr Lys Asp Pro Leu Gly Gln
155 160 165

Thr Glu Lys Ile Tyr Val Leu Asp Gly Thr Gln Asn Asp Thr Ala
170 175 180

Phe Val Phe Pro Arg Leu Arg Asp Phe Thr Leu Ala Met Ala Ala
185 190 195

Arg Lys Ala Ser Arg Val Arg Val Pro Phe Pro Trp Val Gly Thr
200 205 210

Gly Gln Leu Val Tyr Gly Gly Phe Leu Tyr Phe Ala Arg Arg Pro
215 220 225

Pro Gly Arg Pro Gly Gly Gly Gly Glu Met Glu Asn Thr Leu Gln
230 235 240

Leu Ile Lys Phe His Leu Ala Asn Arg Thr Val Val Asp Ser Ser
245 250 255

	230		235		240
Gly Ile Leu Cys	Cys Gly Leu Phe Phe	Gly Ile Val Gly Leu Lys			
	245		250		255
Ile Phe Phe Ser	Lys Phe Gln Trp Lys	Ile Gln Ala Glu Leu Asp			
	260		265		270
Trp Arg Arg Lys	His Gly Gln Ala Glu	Leu Arg Asp Ala Arg Lys			
	275		280		285
His Ala Val Glu	Val Thr Leu Asp Pro	Glu Thr Ala His Pro Lys			
	290		295		300
Leu Cys Val Ser	Asp Leu Lys Thr Val	Thr His Arg Lys Ala Pro			
	305		310		315
Gln Glu Val Pro	His Ser Glu Lys Arg	Phe Thr Arg Lys Ser Val			
	320		325		330
Val Ala Ser Gln	Ser Phe Gln Ala Gly	Lys His Tyr Trp Glu Val			
	335		340		345
Asp Gly Gly His	Asn Lys Arg Trp Arg	Val Gly Val Cys Arg Asp			
	350		355		360
Asp Val Asp Arg	Arg Lys Glu Tyr Val	Thr Leu Ser Pro Asp His			
	365		370		375
Gly Tyr Trp Val	Leu Arg Leu Asn Gly	Glu His Leu Tyr Phe Thr			
	380		385		390
Leu Asn Pro Arg	Phe Ile Ser Val Phe	Pro Arg Thr Pro Pro Thr			
	395		400		405
Lys Ile Gly Val	Phe Leu Asp Tyr Glu	Cys Gly Thr Ile Ser Phe			
	410		415		420
Phe Asn Ile Asn	Asp Gln Ser Leu Ile	Tyr Thr Leu Thr Cys Arg			
	425		430		435
Phe Glu Gly Leu	Leu Arg Pro Tyr Ile	Glu Tyr Pro Ser Tyr Asn			
	440		445		450
Glu Gln Asn Gly	Thr Pro Ile Val Ile	Cys Pro Val Thr Gln Glu			
	455		460		465
Ser Glu Lys Glu	Ala Ser Trp Gln Arg	Ala Ser Ala Ile Pro Glu			
	470		475		480
Thr Ser Asn Ser	Glu Ser Ser Ser Gln	Ala Thr Thr Pro Phe Leu			
	485		490		495
Pro Arg Gly Glu	Met				
	500				

<210> 149

<211> 24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 149
gcgtggtcca cctctacagg gacg 24

<210> 150
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 150
ggaactgacc cagtgtgac acc 23

<210> 151
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 151
gcagatgccca cagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152
<211> 2294
<212> DNA
<213> Homo sapiens

<400> 152
gcgatggtgc gcccggtggc ggtggcggcg gcggttgccg aggcttcctt 50
ggtcggattg caacgaggag aagatgactg accaaccgac tggctgaatg 100
aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctgggcg 150
gcctcgccct gttgtgctgc gccgcgcgcg ccgcccgcgt cgcctcagcc 200
gcctcggcgg ggaatgtcac cgggtggcggc gggggcgcgg ggcaggtgga 250
cgcgtcgccg ggccccgggt tgcggggcga gccagccac cccttccta 300
gggcgacggc tcccacggcc caggccccga ggaccgggccc cccgcgcgcc 350
accgtccacc gaccctggc tgcgacttct ccagcccagt ccccgagac 400

cacccctctt tgggcgactg ctggaccctc ttccaccacc tttcaggcgc 450
cgctcggccc ctgcgcgacc acccctccgg cggcggaacg cacttcgacc 500
acctctcagg cgccgaccag acccgcgcgg accacccttt cgacgaccac 550
tggcccggcg ccgaccaccc ctgtagcgac caccgtaccg gcgcccacga 600
ctccccggac ccgaccccc gatctcccca gcagcagcaa cagcagcgtc 650
ctccccaccc cacctgccac cgaggccccc tcttcgcctc ctccagagta 700
tgtatgtaac tgctctgtgg ttggaagcct gaatgtgaat cgctgcaacc 750
agaccacagg gcagtgtgag tgtcggccag gttatcaggg gcttactgt 800
gaaacctgca aagagggtt ttacctaaat tacacttctg ggctctgtca 850
gccatgtgac tgtagtccac atggagctct cagcataccg tgcaacaggt 900
aagcaacaga ggggtggaact gaagtttatt ttattttagc aagggaacaa 950
aaaaggctgc tactctcaag gaccatactg gtttaaacaaggaggatga 1000
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atgttatatt taatgtcagg atttaaaaac atctaattta ctgatttagt 1100
tcttcaaaag cactagagtc gccaatTTTT ctctgggata atttctgtaa 1150
atttcatggg aaaaaattat tgaagaataa atctgcttcc tggaagggt 1200
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atataccatt ggagtttgag gaaatttggt gtttggttta tttttctctc 1300
taatcaaaat tctacatttg tttctttgga catctaaagc ttaacctggg 1350
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taccagtaca ttttgagac caaaagtaga ttaagcagga attatcttta 1450
aactattatg ttatttgag gtaatttaat ctagtggaat aatgtactgt 1500
tatctaagca ttgacctgt actgcactga aagtaattat tctttgacct 1550
tatgtgaggc acttggttt ttgtggaccc caagtcaaaa aactgaagag 1600
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ctggtttgtt ttaatttcaa aggaatatta tggactgaaa tgagagaaca 1850

tgttttaaga acttttagct ccttgacaaa gaagtgcctt atactttagc 1900
 actaaatatt ttaaagtctt tataaatgat attatactgt tatggaatat 1950
 tgtatcatat tgtagtttat taaaaatgta gaagaggctg ggcgcggtgg 2000
 ctcacgcctg taatcctagc actttgggag gccaaaggcg gtggatcact 2050
 tgaggccagg agttctagat gagcctggcc agcacagtga aaccccgctc 2100
 ctactaaaaa tacaaacaaa ttagctgggc gtggtggcac acacctgtag 2150
 tcccagctac tcgggaggct gaggcaggag aatcggttga acccgggagg 2200
 tggaggttgc agtgagctga gatcgcgcca ctgcactcca gcctggtgag 2250
 agagggagac tctgtottaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153
 <211> 258
 <212> PRT
 <213> Homo sapiens

<400> 153
 Met Arg Ser Leu Pro Ser Leu Gly Gly Leu Ala Leu Leu Cys Cys
 1 5 10 15
 Ala Ala Ala Ala Ala Val Ala Ser Ala Ala Ser Ala Gly Asn
 20 25 30
 Val Thr Gly Gly Gly Gly Ala Ala Gly Gln Val Asp Ala Ser Pro
 35 40 45
 Gly Pro Gly Leu Arg Gly Glu Pro Ser His Pro Phe Pro Arg Ala
 50 55 60
 Thr Ala Pro Thr Ala Gln Ala Pro Arg Thr Gly Pro Pro Arg Ala
 65 70 75
 Thr Val His Arg Pro Leu Ala Ala Thr Ser Pro Ala Gln Ser Pro
 80 85 90
 Glu Thr Thr Pro Leu Trp Ala Thr Ala Gly Pro Ser Ser Thr Thr
 95 100 105
 Phe Gln Ala Pro Leu Gly Pro Ser Pro Thr Thr Pro Pro Ala Ala
 110 115 120
 Glu Arg Thr Ser Thr Thr Ser Gln Ala Pro Thr Arg Pro Ala Pro
 125 130 135
 Thr Thr Leu Ser Thr Thr Thr Gly Pro Ala Pro Thr Thr Pro Val
 140 145 150
 Ala Thr Thr Val Pro Ala Pro Thr Thr Pro Arg Thr Pro Thr Pro
 155 160 165
 Asp Leu Pro Ser Ser Ser Asn Ser Ser Val Leu Pro Thr Pro Pro

Arg	Asn	Ser	Gly	Trp	Val	Phe	Glu	Asn	Pro	Ser	Ile	Gly	Val	Leu
				95					100					105
Glu	Leu	Trp	Val	Leu	Ala	Thr	Asn	Phe	Arg	Asp	Tyr	Ala	Ile	Ile
				110					115					120
Phe	Thr	Gln	Leu	Glu	Phe	Gly	Asp	Glu	Pro	Phe	Asn	Thr	Val	Glu
				125					130					135
Leu	Tyr	Ser	Leu	Thr	Glu	Thr	Ala	Ser	Gln	Glu	Ala	Met	Gly	Leu
				140					145					150
Phe	Thr	Lys	Trp	Ser	Arg	Ser	Leu	Gly	Phe	Leu	Ser	Gln		
				155					160					

<210> 159

<211> 1665

<212> DNA

<213> Homo sapiens

<400> 159

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aacagacgtt ccctcgcggc cctggcacct ctaaccccag acatgctgct 50
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gtaaactgct gacgatgcag agttccgtga cggtgcagga aggcctgtgt 150
gtccatgtgc cctgctcctt ctccacccc tcgcatggct ggatttacct 200
tggcccagta gttcatggct actggttccg ggaaggggcc aatacagacc 250
aggatgctcc agtggccaca aacaaccag ctcgggcagt gtgggaggag 300
actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350
cctgagcatc agagatgcca gaagaagtga tgcggggaga tacttctttc 400
gtatggagaa aggaagtata aaatggaatt ataaacatca ccggctctct 450
gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500
cctggagtcc ggctgcccc agaatctgac ctgctctgtg ccctgggcct 550
gtgagcaggg gacaccccct atgatctcct ggatagggac ctccgtgtcc 600
cccctggacc cctccaccac ccgctcctcg gtgctcacc tcacccaca 650
gccccaggac catggcacca gcctcacctg tcaggtgacc ttccctgggg 700
ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctacccgcct 750
cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800
cttgggaaat ggctcatctc tgtcactccc agagggccag tctctgcgcc 850
tggtctgtgc agttgatgca gttgacagca atccccctgc caggctgagc 900
ctgagctgga gaggcctgac cctgtgcccc tcacagccct caaaccggg 950

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					110					115					120
Met	Glu	Lys	Gly		Ser 125	Ile	Lys	Trp	Asn	Tyr 130	Lys	His	His	Arg	Leu 135
Ser	Val	Asn	Val		Thr 140	Ala	Leu	Thr	His	Arg 145	Pro	Asn	Ile	Leu	Ile 150
Pro	Gly	Thr	Leu		Glu 155	Ser	Gly	Cys	Pro	Gln 160	Asn	Leu	Thr	Cys	Ser 165
Val	Pro	Trp	Ala		Cys 170	Glu	Gln	Gly	Thr	Pro 175	Pro	Met	Ile	Ser	Trp 180
Ile	Gly	Thr	Ser		Val 185	Ser	Pro	Leu	Asp	Pro 190	Ser	Thr	Thr	Arg	Ser 195
Ser	Val	Leu	Thr		Leu 200	Ile	Pro	Gln	Pro	Gln 205	Asp	His	Gly	Thr	Ser 210
Leu	Thr	Cys	Gln		Val 215	Thr	Phe	Pro	Gly	Ala 220	Ser	Val	Thr	Thr	Asn 225
Lys	Thr	Val	His		Leu 230	Asn	Val	Ser	Tyr	Pro 235	Pro	Gln	Asn	Leu	Thr 240
Met	Thr	Val	Phe		Gln 245	Gly	Asp	Gly	Thr	Val 250	Ser	Thr	Val	Leu	Gly 255
Asn	Gly	Ser	Ser		Leu 260	Ser	Leu	Pro	Glu	Gly 265	Gln	Ser	Leu	Arg	Leu 270
Val	Cys	Ala	Val		Asp 275	Ala	Val	Asp	Ser	Asn 280	Pro	Pro	Ala	Arg	Leu 285
Ser	Leu	Ser	Trp		Arg 290	Gly	Leu	Thr	Leu	Cys 295	Pro	Ser	Gln	Pro	Ser 300
Asn	Pro	Gly	Val		Leu 305	Glu	Leu	Pro	Trp	Val 310	His	Leu	Arg	Asp	Ala 315
Ala	Glu	Phe	Thr		Cys 320	Arg	Ala	Gln	Asn	Pro 325	Leu	Gly	Ser	Gln	Gln 330
Val	Tyr	Leu	Asn		Val 335	Ser	Leu	Gln	Ser	Lys 340	Ala	Thr	Ser	Gly	Val 345
Thr	Gln	Gly	Val		Val 350	Gly	Gly	Ala	Gly	Ala 355	Thr	Ala	Leu	Val	Phe 360
Leu	Ser	Phe	Cys		Val 365	Ile	Phe	Val	Val	Val 370	Arg	Ser	Cys	Arg	Lys 375
Lys	Ser	Ala	Arg		Pro 380	Ala	Ala	Gly	Val	Gly 385	Asp	Thr	Gly	Ile	Glu 390
Asp	Ala	Asn	Ala		Val 395	Arg	Gly	Ser	Ala	Ser 400	Gln	Gly	Pro	Leu	Thr 405

Glu	Pro	Trp	Ala	Glu	Asp	Ser	Pro	Pro	Asp	Gln	Pro	Pro	Pro	Ala
				410					415					420
Ser	Ala	Arg	Ser	Ser	Val	Gly	Glu	Gly	Glu	Leu	Gln	Tyr	Ala	Ser
				425					430					435
Leu	Ser	Phe	Gln	Met	Val	Lys	Pro	Trp	Asp	Ser	Arg	Gly	Gln	Glu
				440					445					450
Ala	Thr	Asp	Thr	Glu	Tyr	Ser	Glu	Ile	Lys	Ile	His	Arg		
				455					460					

<210> 161
 <211> 739
 <212> DNA
 <213> Homo sapiens

<400> 161
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 accctgttcc tgggtgtcac gctcggcctg gccgctgccc tgtccttcac 100
 cctggaggag gaggatatca cagggaacctg gtacgtgaag gccatggtgg 150
 tcgataagga ctttccggag gacaggaggc ccaggaaggt gtccccagtg 200
 aaggtgacag ccctgggcgg tgggaagttg gaagccacgt tcaccttcat 250
 gagggaggat cgggtgcatcc agaagaaaat cctgatgcgg aagacggagg 300
 agcctggcaa atacagcgcc tatgggggca ggaagctcat gtacctgcag 350
 gagctgcccc ggagggacca ctacatcttt tactgcaaag accagacca 400
 tgggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450
 accgggaggc cctggaagaa tttaagaaat tgggtgcagcg caagggactc 500
 tcggaggagg acattttcac gccctgcag acgggaagct gcgttcccg 550
 aactaggca gccccgggt ctgcacctcc agagcccacc ctaccaccag 600
 acacagagcc cggaccacct ggacctaccc tccagccatg acccttccct 650
 gctcccaccc acctgactcc aaataaagtc cttttcccc aaaaaaaaaa 700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 162
 Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala
 1 5 10 15
 Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr

20					25					30				
Val	Lys	Ala	Met	Val	Val	Asp	Lys	Asp	Phe	Pro	Glu	Asp	Arg	Arg
			35						40					45
Pro	Arg	Lys	Val	Ser	Pro	Val	Lys	Val	Thr	Ala	Leu	Gly	Gly	Gly
			50						55					60
Lys	Leu	Glu	Ala	Thr	Phe	Thr	Phe	Met	Arg	Glu	Asp	Arg	Cys	Ile
			65						70					75
Gln	Lys	Lys	Ile	Leu	Met	Arg	Lys	Thr	Glu	Glu	Pro	Gly	Lys	Tyr
			80						85					90
Ser	Ala	Tyr	Gly	Gly	Arg	Lys	Leu	Met	Tyr	Leu	Gln	Glu	Leu	Pro
			95						100					105
Arg	Arg	Asp	His	Tyr	Ile	Phe	Tyr	Cys	Lys	Asp	Gln	His	His	Gly
			110						115					120
Gly	Leu	Leu	His	Met	Gly	Lys	Leu	Val	Gly	Arg	Asn	Ser	Asp	Thr
			125						130					135
Asn	Arg	Glu	Ala	Leu	Glu	Glu	Phe	Lys	Lys	Leu	Val	Gln	Arg	Lys
			140						145					150
Gly	Leu	Ser	Glu	Glu	Asp	Ile	Phe	Thr	Pro	Leu	Gln	Thr	Gly	Ser
			155						160					165
Cys	Val	Pro	Glu	His										
			170											

<210> 163
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 163
 ggagatgaag accctgttcc tg 22

<210> 164
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 164
 ggagatgaag accctgttcc tgggtg 26

Val	Gly	Gly	Glu	Thr	Arg	Ile	Ile	Lys	Gly	Phe	Glu	Cys	Lys	Pro	20	25	30
His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Phe	Glu	Lys	Thr	Arg	Leu	35	40	45
Leu	Cys	Gly	Ala	Thr	Leu	Ile	Ala	Pro	Arg	Trp	Leu	Leu	Thr	Ala	50	55	60
Ala	His	Cys	Leu	Lys	Pro	Arg	Tyr	Ile	Val	His	Leu	Gly	Gln	His	65	70	75
Asn	Leu	Gln	Lys	Glu	Glu	Gly	Cys	Glu	Gln	Thr	Arg	Thr	Ala	Thr	80	85	90
Glu	Ser	Phe	Pro	His	Pro	Gly	Phe	Asn	Asn	Ser	Leu	Pro	Asn	Lys	95	100	105
Asp	His	Arg	Asn	Asp	Ile	Met	Leu	Val	Lys	Met	Ala	Ser	Pro	Val	110	115	120
Ser	Ile	Thr	Trp	Ala	Val	Arg	Pro	Leu	Thr	Leu	Ser	Ser	Arg	Cys	125	130	135
Val	Thr	Ala	Gly	Thr	Ser	Cys	Leu	Ile	Ser	Gly	Trp	Gly	Ser	Thr	140	145	150
Ser	Ser	Pro	Gln	Leu	Arg	Leu	Pro	His	Thr	Leu	Arg	Cys	Ala	Asn	155	160	165
Ile	Thr	Ile	Ile	Glu	His	Gln	Lys	Cys	Glu	Asn	Ala	Tyr	Pro	Gly	170	175	180
Asn	Ile	Thr	Asp	Thr	Met	Val	Cys	Ala	Ser	Val	Gln	Glu	Gly	Gly	185	190	195
Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn	200	205	210
Gln	Ser	Leu	Gln	Gly	Ile	Ile	Ser	Trp	Gly	Gln	Asp	Pro	Cys	Ala	215	220	225
Ile	Thr	Arg	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Cys	Lys	Tyr	Val	230	235	240
Asp	Trp	Ile	Gln	Glu	Thr	Met	Lys	Asn	Asn						245	250	

<210> 171

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-25

<223> Synthetic construct.

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 176

cccttgatga tcctgggc 18

<210> 177

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 177

aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 50

<210> 178

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 178

gagagaccag gatcatcaag gggttcgagt gcaagcctca ctc 43

<210> 179

<211> 907

<212> DNA

<213> Homo sapiens

<400> 179

gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50

gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100

aagaaagagg agagcaccga agaagtgaaa atagaagttt tgcacgtcc 150

agaaaactgc tctaagacaa gcaagaagg agacctacta aatgcccatt 200

atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250

caaaatgaag gccaccccaa atggtttggt cttggtgttg ggcaagtcac 300

aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350

aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400

Ile	Glu	Thr	Phe	Lys	Gln	Ile	Asp	Met	Asp	Asn	Asp	Arg	Gln	Leu
				155					160					165
Ser	Lys	Ala	Glu	Ile	Asn	Leu	Tyr	Leu	Gln	Arg	Glu	Phe	Glu	Lys
				170					175					180
Asp	Glu	Lys	Pro	Arg	Asp	Lys	Ser	Tyr	Gln	Asp	Ala	Val	Leu	Glu
				185					190					195
Asp	Ile	Phe	Lys	Lys	Asn	Asp	His	Asp	Gly	Asp	Gly	Phe	Ile	Ser
				200					205					210
Pro	Lys	Glu	Tyr	Asn	Val	Tyr	Gln	His	Asp	Glu	Leu			
				215					220					

<210> 181
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 181
 gtgttctgct ggagccgatg cc 22

<210> 182
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 182
 gacatggaca atgacagg 18

<210> 183
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 183
 cctttcagga tgtaggag 18

<210> 184
 <211> 18
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 184
gatgtctgcc accccaag 18

<210> 185
<211> 27
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-27
<223> Synthetic construct.

<400> 185
gcatcctgat atgacttgtc acgtggc 27

<210> 186
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 186
tacaagaggg aagaggagtt gcac 24

<210> 187
<211> 52
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-52
<223> Synthetic construct.

<400> 187
gccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50
cc 52

<210> 188
<211> 573
<212> DNA
<213> Homo sapiens

<400> 188
cagaaatgca gggaccattg cttcttccag gcctctgctt tctgctgagc 50
ctctttggag ctgtgactca gaaaaccaa acttcctgtg ctaagtgcc 100

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 191
cgttacatgt ctccaagggg aatg 24

<210> 192
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 192
cctgtgctaa gtgccccca aatgcttct gtgtcaataa cactcactgc 50

<210> 193
<211> 1091
<212> DNA
<213> Homo sapiens

<400> 193
caagcaggtc atccccttgg tgaccttcaa agagaagcag agagggcaga 50
ggtggggggc acagggaaag ggtgacctct gagattcccc ttttccccca 100
gactttggaa gtgaccacc atggggctca gcatcttttt gctcctgtgt 150
gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200
gtgtgggctg aactcacagc cgtggcaggt ggggctgttt gagggcacca 250
gcctgcgctg cgggggtgtc cttattgacc acaggtgggt cctcacagcg 300
gctcactgca gcggcagcag gtactgggtg cgctggggg aacacagcct 350
cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400
cccatcccgg ctacctggga gctcgcgca gccacgagca cgacctccgg 450
ctgctgcggc tgcgcctgcc cgtccgcgta accagcagcg ttcaaccocct 500
gcccctgccc aatgactgtg caaccgctgg caccgagtgc cagctctcag 550
gctggggcat caccaaccac ccacggaacc cattcccga tctgctocag 600
tgctcaacc tctccatcgt ctcccatgcc acctgccatg gtgtgtatcc 650
cgggagaatc acgagcaaca tgggtgtgtc aggcggcgtc ccggggcagg 700
atgcctgcca gggtgattct gggggcccc tgggtgtgtg gggagtcctt 750
caaggtctgg tgtcctgggg gtctgtgggg cctgtggac aagatggcat 800

ccctggagtc tacacctata tttgcaagta tgtggactgg atccggatga 850
 tcatgaggaa caactgacct gtttcctcca cctccacccc cacccttaa 900
 cttgggtacc cctctggccc tcagagcacc aatatctcct ccatcacttc 950
 ccctagctcc actcttgttg gcctgggaac ttcttggaac tttaactcct 1000
 gccagccctt ctaagaccca cgagcggggg gagagaagtg tgcaatagtc 1050
 tggaataaat ataaatgaag gaggggcaaa aaaaaaaaaa a 1091

<210> 194

<211> 248

<212> PRT

<213> Homo sapiens

<400> 194

Met	Gly	Leu	Ser	Ile	Phe	Leu	Leu	Leu	Cys	Val	Leu	Gly	Leu	Ser	1	5	10	15
Gln	Ala	Ala	Thr	Pro	Lys	Ile	Phe	Asn	Gly	Thr	Glu	Cys	Gly	Arg	20	25	30	
Asn	Ser	Gln	Pro	Trp	Gln	Val	Gly	Leu	Phe	Glu	Gly	Thr	Ser	Leu	35	40	45	
Arg	Cys	Gly	Gly	Val	Leu	Ile	Asp	His	Arg	Trp	Val	Leu	Thr	Ala	50	55	60	
Ala	His	Cys	Ser	Gly	Ser	Arg	Tyr	Trp	Val	Arg	Leu	Gly	Glu	His	65	70	75	
Ser	Leu	Ser	Gln	Leu	Asp	Trp	Thr	Glu	Gln	Ile	Arg	His	Ser	Gly	80	85	90	
Phe	Ser	Val	Thr	His	Pro	Gly	Tyr	Leu	Gly	Ala	Ser	Thr	Ser	His	95	100	105	
Glu	His	Asp	Leu	Arg	Leu	Leu	Arg	Leu	Arg	Leu	Pro	Val	Arg	Val	110	115	120	
Thr	Ser	Ser	Val	Gln	Pro	Leu	Pro	Leu	Pro	Asn	Asp	Cys	Ala	Thr	125	130	135	
Ala	Gly	Thr	Glu	Cys	His	Val	Ser	Gly	Trp	Gly	Ile	Thr	Asn	His	140	145	150	
Pro	Arg	Asn	Pro	Phe	Pro	Asp	Leu	Leu	Gln	Cys	Leu	Asn	Leu	Ser	155	160	165	
Ile	Val	Ser	His	Ala	Thr	Cys	His	Gly	Val	Tyr	Pro	Gly	Arg	Ile	170	175	180	
Thr	Ser	Asn	Met	Val	Cys	Ala	Gly	Gly	Val	Pro	Gly	Gln	Asp	Ala	185	190	195	
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gly	Gly	Val	Leu				

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 attccacacc tcttctcatc ctcaagtatg tgaaggtggg aaggaaagga 1150
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 ctgctctctg gccacacctg tgcaggcagc tgagaggcag cgtgcagccc 1250
 tactgtccct tactggggca gcagagggct tcggaggcag aagtgaggcc 1300
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 gatactgagg ggaccaggat gggagaatga ggagtaaaat gctcacggca 1400
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<210> 196

<211> 150

<212> PRT

<213> Homo sapiens

<400> 196

Met	Ser	Gly	Glu	Leu	Ser	Asn	Arg	Phe	Gln	Gly	Gly	Lys	Ala	Phe
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Gly	Leu	Leu	Lys	Ala	Arg	Gln	Glu	Arg	Arg	Leu	Ala	Glu	Ile	Asn
				20					25					30

Arg	Glu	Phe	Leu	Cys	Asp	Gln	Lys	Tyr	Ser	Asp	Glu	Glu	Asn	Leu
				35					40					45

Pro	Glu	Lys	Leu	Thr	Ala	Phe	Lys	Glu	Lys	Tyr	Met	Glu	Phe	Asp
				50					55					60

Leu	Asn	Asn	Glu	Gly	Glu	Ile	Asp	Leu	Met	Ser	Leu	Lys	Arg	Met
				65					70					75

Met	Glu	Lys	Leu	Gly	Val	Pro	Lys	Thr	His	Leu	Glu	Met	Lys	Lys
				80					85					90

Met	Ile	Ser	Glu	Val	Thr	Gly	Gly	Val	Ser	Asp	Thr	Ile	Ser	Tyr
				95					100					105

Arg	Asp	Phe	Val	Asn	Met	Met	Leu	Gly	Lys	Arg	Ser	Ala	Val	Leu
				110					115					120

Lys	Leu	Val	Met	Met	Phe	Glu	Gly	Lys	Ala	Asn	Glu	Ser	Ser	Pro
				125					130					135

Lys	Pro	Val	Gly	Pro	Pro	Pro	Glu	Arg	Asp	Ile	Ala	Ser	Leu	Pro
				140					145					150

<210> 197

<211> 4842

<212> DNA

<213> Homo sapiens

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tgacagccac aaggatgggt tcagctgctc ctgccctctg ggctttgagg 3050
ggcagcgggtg tgagatcaac ccagatgact gtgaggacaa cgactgcgaa 3100
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cgaccagtac gagtgccaga acggggccca gtgcatcgtg gtgcagcagg 3500
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cggccacaga tgccaccatg gaaaatgtgt ggcaactggg acctcataca 4250
tgtgcaagtg tgccgagggc tatggagggg acttgtgtga caacaagaat 4300
gactctgcca atgcctgctc agccttcaag tgtcaccatg ggcagtgcc 4350

Asn	Asn	His	Ile	Ser 170	Cys	Ile	Glu	Asp	Gly 175	Ala	Phe	Arg	Ala	Leu 180
Arg	Asp	Leu	Glu	Ile 185	Leu	Thr	Leu	Asn	Asn 190	Asn	Asn	Ile	Ser	Arg 195
Ile	Leu	Val	Thr	Ser 200	Phe	Asn	His	Met	Pro 205	Lys	Ile	Arg	Thr	Leu 210
Arg	Leu	His	Ser	Asn 215	His	Leu	Tyr	Cys	Asp 220	Cys	His	Leu	Ala	Trp 225
Leu	Ser	Asp	Trp	Leu 230	Arg	Gln	Arg	Arg	Thr 235	Val	Gly	Gln	Phe	Thr 240
Leu	Cys	Met	Ala	Pro 245	Val	His	Leu	Arg	Gly 250	Phe	Asn	Val	Ala	Asp 255
Val	Gln	Lys	Lys	Glu 260	Tyr	Val	Cys	Pro	Ala 265	Pro	His	Ser	Glu	Pro 270
Pro	Ser	Cys	Asn	Ala 275	Asn	Ser	Ile	Ser	Cys 280	Pro	Ser	Pro	Cys	Thr 285
Cys	Ser	Asn	Asn	Ile 290	Val	Asp	Cys	Arg	Gly 295	Lys	Gly	Leu	Met	Glu 300
Ile	Pro	Ala	Asn	Leu 305	Pro	Glu	Gly	Ile	Val 310	Glu	Ile	Arg	Leu	Glu 315
Gln	Asn	Ser	Ile	Lys 320	Ala	Ile	Pro	Ala	Gly 325	Ala	Phe	Thr	Gln	Tyr 330
Lys	Lys	Leu	Lys	Arg 335	Ile	Asp	Ile	Ser	Lys 340	Asn	Gln	Ile	Ser	Asp 345
Ile	Ala	Pro	Asp	Ala 350	Phe	Gln	Gly	Leu	Lys 355	Ser	Leu	Thr	Ser	Leu 360
Val	Leu	Tyr	Gly	Asn 365	Lys	Ile	Thr	Glu	Ile 370	Ala	Lys	Gly	Leu	Phe 375
Asp	Gly	Leu	Val	Ser 380	Leu	Gln	Leu	Leu	Leu 385	Leu	Asn	Ala	Asn	Lys 390
Ile	Asn	Cys	Leu	Arg 395	Val	Asn	Thr	Phe	Gln 400	Asp	Leu	Gln	Asn	Leu 405
Asn	Leu	Leu	Ser	Leu 410	Tyr	Asp	Asn	Lys	Leu 415	Gln	Thr	Ile	Ser	Lys 420
Gly	Leu	Phe	Ala	Pro 425	Leu	Gln	Ser	Ile	Gln 430	Thr	Leu	His	Leu	Ala 435
Gln	Asn	Pro	Phe	Val 440	Cys	Asp	Cys	His	Leu 445	Lys	Trp	Leu	Ala	Asp 450
Tyr	Leu	Gln	Asp	Asn	Pro	Ile	Glu	Thr	Ser	Gly	Ala	Arg	Cys	Ser

				455					460					465
Ser	Pro	Arg	Arg	Leu 470	Ala	Asn	Lys	Arg	Ile 475	Ser	Gln	Ile	Lys	Ser 480
Lys	Lys	Phe	Arg	Cys 485	Ser	Gly	Ser	Glu	Asp 490	Tyr	Arg	Ser	Arg	Phe 495
Ser	Ser	Glu	Cys	Phe 500	Met	Asp	Leu	Val	Cys 505	Pro	Glu	Lys	Cys	Arg 510
Cys	Glu	Gly	Thr	Ile 515	Val	Asp	Cys	Ser	Asn 520	Gln	Lys	Leu	Val	Arg 525
Ile	Pro	Ser	His	Leu 530	Pro	Glu	Tyr	Val	Thr 535	Asp	Leu	Arg	Leu	Asn 540
Asp	Asn	Glu	Val	Ser 545	Val	Leu	Glu	Ala	Thr 550	Gly	Ile	Phe	Lys	Lys 555
Leu	Pro	Asn	Leu	Arg 560	Lys	Ile	Asn	Leu	Ser 565	Asn	Asn	Lys	Ile	Lys 570
Glu	Val	Arg	Glu	Gly 575	Ala	Phe	Asp	Gly	Ala 580	Ala	Ser	Val	Gln	Glu 585
Leu	Met	Leu	Thr	Gly 590	Asn	Gln	Leu	Glu	Thr 595	Val	His	Gly	Arg	Val 600
Phe	Arg	Gly	Leu	Ser 605	Gly	Leu	Lys	Thr	Leu 610	Met	Leu	Arg	Ser	Asn 615
Leu	Ile	Ser	Cys	Val 620	Ser	Asn	Asp	Thr	Phe 625	Ala	Gly	Leu	Ser	Ser 630
Val	Arg	Leu	Leu	Ser 635	Leu	Tyr	Asp	Asn	Arg 640	Ile	Thr	Thr	Ile	Thr 645
Pro	Gly	Ala	Phe	Thr 650	Thr	Leu	Val	Ser	Leu 655	Ser	Thr	Ile	Asn	Leu 660
Leu	Ser	Asn	Pro	Phe 665	Asn	Cys	Asn	Cys	His 670	Leu	Ala	Trp	Leu	Gly 675
Lys	Trp	Leu	Arg	Lys 680	Arg	Arg	Ile	Val	Ser 685	Gly	Asn	Pro	Arg	Cys 690
Gln	Lys	Pro	Phe	Phe 695	Leu	Lys	Glu	Ile	Pro 700	Ile	Gln	Asp	Val	Ala 705
Ile	Gln	Asp	Phe	Thr 710	Cys	Asp	Gly	Asn	Glu 715	Glu	Ser	Ser	Cys	Gln 720
Leu	Ser	Pro	Arg	Cys 725	Pro	Glu	Gln	Cys	Thr 730	Cys	Met	Glu	Thr	Val 735
Val	Arg	Cys	Ser	Asn 740	Lys	Gly	Leu	Arg	Ala 745	Leu	Pro	Arg	Gly	Met 750

Pro Lys Asp Val	Thr Glu Leu Tyr Leu	Glu Gly Asn His Leu	Thr
	755	760	765
Ala Val Pro Arg	Glu Leu Ser Ala Leu	Arg His Leu Thr Leu	Ile
	770	775	780
Asp Leu Ser Asn	Asn Ser Ile Ser Met	Leu Thr Asn Tyr Thr	Phe
	785	790	795
Ser Asn Met Ser	His Leu Ser Thr Leu	Ile Leu Ser Tyr Asn	Arg
	800	805	810
Leu Arg Cys Ile	Pro Val His Ala Phe	Asn Gly Leu Arg Ser	Leu
	815	820	825
Arg Val Leu Thr	Leu His Gly Asn Asp	Ile Ser Ser Val Pro	Glu
	830	835	840
Gly Ser Phe Asn	Asp Leu Thr Ser Leu	Ser His Leu Ala Leu	Gly
	845	850	855
Thr Asn Pro Leu	His Cys Asp Cys Ser	Leu Arg Trp Leu Ser	Glu
	860	865	870
Trp Val Lys Ala	Gly Tyr Lys Glu Pro	Gly Ile Ala Arg Cys	Ser
	875	880	885
Ser Pro Glu Pro	Met Ala Asp Arg Leu	Leu Leu Thr Thr Pro	Thr
	890	895	900
His Arg Phe Gln	Cys Lys Gly Pro Val	Asp Ile Asn Ile Val	Ala
	905	910	915
Lys Cys Asn Ala	Cys Leu Ser Ser Pro	Cys Lys Asn Asn Gly	Thr
	920	925	930
Cys Thr Gln Asp	Pro Val Glu Leu Tyr	Arg Cys Ala Cys Pro	Tyr
	935	940	945
Ser Tyr Lys Gly	Lys Asp Cys Thr Val	Pro Ile Asn Thr Cys	Ile
	950	955	960
Gln Asn Pro Cys	Gln His Gly Gly Thr	Cys His Leu Ser Asp	Ser
	965	970	975
His Lys Asp Gly	Phe Ser Cys Ser Cys	Pro Leu Gly Phe Glu	Gly
	980	985	990
Gln Arg Cys Glu	Ile Asn Pro Asp Asp	Cys Glu Asp Asn Asp	Cys
	995	1000	1005
Glu Asn Asn Ala	Thr Cys Val Asp Gly	Ile Asn Asn Tyr Val	Cys
	1010	1015	1020
Ile Cys Pro Pro	Asn Tyr Thr Gly Glu	Leu Cys Asp Glu Val	Ile
	1025	1030	1035
Asp His Cys Val	Pro Glu Leu Asn Leu	Cys Gln His Glu Ala	Lys

				1040					1045					1050
Cys	Ile	Pro	Leu	Asp	Lys	Gly	Phe	Ser	Cys	Glu	Cys	Val	Pro	Gly
				1055					1060					1065
Tyr	Ser	Gly	Lys	Leu	Cys	Glu	Thr	Asp	Asn	Asp	Asp	Cys	Val	Ala
				1070					1075					1080
His	Lys	Cys	Arg	His	Gly	Ala	Gln	Cys	Val	Asp	Thr	Ile	Asn	Gly
				1085					1090					1095
Tyr	Thr	Cys	Thr	Cys	Pro	Gln	Gly	Phe	Ser	Gly	Pro	Phe	Cys	Glu
				1100					1105					1110
His	Pro	Pro	Pro	Met	Val	Leu	Leu	Gln	Thr	Ser	Pro	Cys	Asp	Gln
				1115					1120					1125
Tyr	Glu	Cys	Gln	Asn	Gly	Ala	Gln	Cys	Ile	Val	Val	Gln	Gln	Glu
				1130					1135					1140
Pro	Thr	Cys	Arg	Cys	Pro	Pro	Gly	Phe	Ala	Gly	Pro	Arg	Cys	Glu
				1145					1150					1155
Lys	Leu	Ile	Thr	Val	Asn	Phe	Val	Gly	Lys	Asp	Ser	Tyr	Val	Glu
				1160					1165					1170
Leu	Ala	Ser	Ala	Lys	Val	Arg	Pro	Gln	Ala	Asn	Ile	Ser	Leu	Gln
				1175					1180					1185
Val	Ala	Thr	Asp	Lys	Asp	Asn	Gly	Ile	Leu	Leu	Tyr	Lys	Gly	Asp
				1190					1195					1200
Asn	Asp	Pro	Leu	Ala	Leu	Glu	Leu	Tyr	Gln	Gly	His	Val	Arg	Leu
				1205					1210					1215
Val	Tyr	Asp	Ser	Leu	Ser	Ser	Pro	Pro	Thr	Thr	Val	Tyr	Ser	Val
				1220					1225					1230
Glu	Thr	Val	Asn	Asp	Gly	Gln	Phe	His	Ser	Val	Glu	Leu	Val	Thr
				1235					1240					1245
Leu	Asn	Gln	Thr	Leu	Asn	Leu	Val	Val	Asp	Lys	Gly	Thr	Pro	Lys
				1250					1255					1260
Ser	Leu	Gly	Lys	Leu	Gln	Lys	Gln	Pro	Ala	Val	Gly	Ile	Asn	Ser
				1265					1270					1275
Pro	Leu	Tyr	Leu	Gly	Gly	Ile	Pro	Thr	Ser	Thr	Gly	Leu	Ser	Ala
				1280					1285					1290
Leu	Arg	Gln	Gly	Thr	Asp	Arg	Pro	Leu	Gly	Gly	Phe	His	Gly	Cys
				1295					1300					1305
Ile	His	Glu	Val	Arg	Ile	Asn	Asn	Glu	Leu	Gln	Asp	Phe	Lys	Ala
				1310					1315					1320
Leu	Pro	Pro	Gln	Ser	Leu	Gly	Val	Ser	Pro	Gly	Cys	Lys	Ser	Cys
				1325					1330					1335

<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 200
ttgttgcat tgaggaggag cagc 24

<210> 201
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 201
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<210> 202
<211> 753
<212> DNA
<213> Homo sapiens

<400> 202
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gaatctgcct tttcagttct gtctccggca ggctttgagg atgaaggctg 150
cgggcattct gaccctcatt ggctgcctgg tcacaggcgc cgagtccaaa 200
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cctgtccgag tggaaaaaag gctgtgaggt ttcttaaact ggaactggac 600
ccaggatgct ttgcagcaac gccctaggat ttgcagtga tgtccaaatg 650
cctgtgtcat cttgtcccgt ttctcccaa tttccttctt caaacttgga 700
gagggaaaat taagctatac ttttaagaaa ataaatattt ccatttaaatt 750
gtc 753

<210> 203
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 203
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 Gly Ala Glu Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile
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 Phe Ser Arg Ala Gly Leu Asp Asn Tyr Trp Gly Phe Ser Leu Gly
 35 40 45
 Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr
 50 55 60
 Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe
 65 70 75
 Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu
 80 85 90
 Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp
 95 100 105
 Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr
 110 115 120
 Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly
 125 130 135
 Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser
 140 145

<210> 204
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 204
 gcaggctttg aggatgaagg ctgc 24

<210> 205
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 205
ctcattgggt gcctgggtcac aggc 24

<210> 206
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 206
ccagtcggac aggtctctcc cctc 24

<210> 207
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 207
tcagtgacca aggctgagca ggcg 24

<210> 208
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 208
ctacactcgt tgcaaactgg caaaaatatt ctcgaggggt ggcctgg 47

<210> 209
<211> 1648
<212> DNA
<213> Homo sapiens

<400> 209
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ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200
gcggaagaag atcctatatt actgtcactt cccagatctg cttctcacca 250

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cacagctgct	gtttttaagg	aaacattcaa	gtccctgtct	cacatagacc	400
ctgatgtcct	ctatccatct	ctaaatgtca	ccagctttga	ctcagttggt	450
cctgaaaagc	tggatgacct	agtccccaag	gggaaaaaat	tcctgctgct	500
ctccatcaac	agatacgaaa	ggaagaaaaa	tctgactttg	gcactggaag	550
ccctagtaca	gctgcgtgga	agattgacat	cccaagattg	ggagaggggt	600
catctgatcg	tggcagggtg	ttatgacgag	agagtcctgg	agaatgtgga	650
acattatcag	gaattgaaga	aaatgggtcca	acagtcgcac	cttggccagt	700
atgtgacctt	cttgagggtct	ttctcagaca	aacagaaaat	ctccctcctc	750
cacagctgca	cgtgtgtgct	ttacacacca	agcaatgagc	actttggcat	800
tgtccctctg	gaagccatgt	acatgcagtg	cccagtcatt	gctgttaatt	850
cgggtggacc	cttggagtoc	attgaccaca	gtgtcacagg	gtttctgtgt	900
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ctttcctata	taccacacct	ccctgtccac	ttttcagaaa	aaccatgtct	1250
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tgtcattcca	tgttcagcag	agtattttta	ttatattttc	tcgggattat	1350
tgctcttctg	tctataaatt	ttgaatgata	ctgtgcctta	attggttttc	1400
atagttttaag	tgtgtatcat	tatcaaagtt	gattaatttg	gottcatagt	1450
ataatgagag	cagggctatt	gtagttccca	gattcaatcc	accgaagtgt	1500
tcaactgtcat	ctgttaggga	atttttgttt	gtcctgtott	tgccctggatc	1550
catagcgaga	gtgctctgta	ttttttttta	gataatttgt	atttttgcac	1600
actgagatat	aataaaaaggt	gtttatcata	aaaaaaaaaa	aaaaaaaaaa	1648

 $\langle 211 \rangle$ 323

<212> PRT
 <213> Homo sapiens

<400> 210

Met	Pro	Leu	Leu	Lys	Leu	Val	His	Gly	Ser	Pro	Leu	Val	Phe	Gly	1	5	10	15
Glu	Lys	Phe	Lys	Leu	Phe	Thr	Leu	Val	Ser	Ala	Cys	Ile	Pro	Val	20	25	30	
Phe	Arg	Leu	Ala	Arg	Arg	Arg	Lys	Lys	Ile	Leu	Phe	Tyr	Cys	His	35	40	45	
Phe	Pro	Asp	Leu	Leu	Leu	Thr	Lys	Arg	Asp	Ser	Phe	Leu	Lys	Arg	50	55	60	
Leu	Tyr	Arg	Ala	Pro	Ile	Asp	Trp	Ile	Glu	Glu	Tyr	Thr	Thr	Gly	65	70	75	
Met	Ala	Asp	Cys	Ile	Leu	Val	Asn	Ser	Gln	Phe	Thr	Ala	Ala	Val	80	85	90	
Phe	Lys	Glu	Thr	Phe	Lys	Ser	Leu	Ser	His	Ile	Asp	Pro	Asp	Val	95	100	105	
Leu	Tyr	Pro	Ser	Leu	Asn	Val	Thr	Ser	Phe	Asp	Ser	Val	Val	Pro	110	115	120	
Glu	Lys	Leu	Asp	Asp	Leu	Val	Pro	Lys	Gly	Lys	Lys	Phe	Leu	Leu	125	130	135	
Leu	Ser	Ile	Asn	Arg	Tyr	Glu	Arg	Lys	Lys	Asn	Leu	Thr	Leu	Ala	140	145	150	
Leu	Glu	Ala	Leu	Val	Gln	Leu	Arg	Gly	Arg	Leu	Thr	Ser	Gln	Asp	155	160	165	
Trp	Glu	Arg	Val	His	Leu	Ile	Val	Ala	Gly	Gly	Tyr	Asp	Glu	Arg	170	175	180	
Val	Leu	Glu	Asn	Val	Glu	His	Tyr	Gln	Glu	Leu	Lys	Lys	Met	Val	185	190	195	
Gln	Gln	Ser	Asp	Leu	Gly	Gln	Tyr	Val	Thr	Phe	Leu	Arg	Ser	Phe	200	205	210	
Ser	Asp	Lys	Gln	Lys	Ile	Ser	Leu	Leu	His	Ser	Cys	Thr	Cys	Val	215	220	225	
Leu	Tyr	Thr	Pro	Ser	Asn	Glu	His	Phe	Gly	Ile	Val	Pro	Leu	Glu	230	235	240	
Ala	Met	Tyr	Met	Gln	Cys	Pro	Val	Ile	Ala	Val	Asn	Ser	Gly	Gly	245	250	255	
Pro	Leu	Glu	Ser	Ile	Asp	His	Ser	Val	Thr	Gly	Phe	Leu	Cys	Glu	260	265	270	

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 gccaaactga ctccagtttc tgcccagctt caagatatg aaggaaaaat 1100
 tgaccgattt attattccta gagagaccct cgtcctttat gcccttggtg 1150
 tggtagttca ggatcctaatt acttggccat ctccacacaa gtttgatcca 1200
 gatcggtttg atgatgaatt agtaatgaaa actttttcct cacttggatt 1250
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 cagtacttct tagtgtattg gtgaagagac tgcacctact ttctgtggag 1350
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 agcttggatc actgtctcaa agagatatta aaattttata catttaaaat 1450
 cattgttaaa ttgattgagg aaaacaacca tttaaaaaaa atctatgttg 1500
 aatcctttta taaaccagta tcactttgta atataaacac ctatttgtac 1550
 ttaa 1554

<210> 212
 <211> 462
 <212> PRT
 <213> Homo sapiens

<400> 212
 Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu Ala Leu
 1 5 10 15
 Val Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala
 20 25 30
 Gly Ile Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu
 35 40 45
 Pro Asp Ile Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn
 50 55 60
 Leu His Glu Arg Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg
 65 70 75
 Arg Leu Val Val Ser Leu Gly Thr Val Asp Val Leu Lys Gln His
 80 85 90
 Ile Asn Pro Asn Lys Thr Ser Asp Pro Phe Glu Thr Met Leu Lys
 95 100 105
 Ser Leu Leu Arg Tyr Gln Ser Gly Gly Gly Ser Val Ser Glu Asn
 110 115 120
 His Met Arg Lys Lys Leu Tyr Glu Asn Gly Val Thr Asp Ser Leu
 125 130 135
 Lys Ser Asn Phe Ala Leu Leu Leu Lys Leu Ser Glu Glu Leu Leu

	140		145		150
Asp Lys Trp Leu Ser Tyr Pro Glu Thr Gln His Val Pro Leu Ser	155		160		165
Gln His Met Leu Gly Phe Ala Met Lys Ser Val Thr Gln Met Val	170		175		180
Met Gly Ser Thr Phe Glu Asp Asp Gln Glu Val Ile Arg Phe Gln	185		190		195
Lys Asn His Gly Thr Val Trp Ser Glu Ile Gly Lys Gly Phe Leu	200		205		210
Asp Gly Ser Leu Asp Lys Asn Met Thr Arg Lys Lys Gln Tyr Glu	215		220		225
Asp Ala Leu Met Gln Leu Glu Ser Val Leu Arg Asn Ile Ile Lys	230		235		240
Glu Arg Lys Gly Arg Asn Phe Ser Gln His Ile Phe Ile Asp Ser	245		250		255
Leu Val Gln Gly Asn Leu Asn Asp Gln Gln Ile Leu Glu Asp Ser	260		265		270
Met Ile Phe Ser Leu Ala Ser Cys Ile Ile Thr Ala Lys Leu Cys	275		280		285
Thr Trp Ala Ile Cys Phe Leu Thr Thr Ser Glu Glu Val Gln Lys	290		295		300
Lys Leu Tyr Glu Glu Ile Asn Gln Val Phe Gly Asn Gly Pro Val	305		310		315
Thr Pro Glu Lys Ile Glu Gln Leu Arg Tyr Cys Gln His Val Leu	320		325		330
Cys Glu Thr Val Arg Thr Ala Lys Leu Thr Pro Val Ser Ala Gln	335		340		345
Leu Gln Asp Ile Glu Gly Lys Ile Asp Arg Phe Ile Ile Pro Arg	350		355		360
Glu Thr Leu Val Leu Tyr Ala Leu Gly Val Val Leu Gln Asp Pro	365		370		375
Asn Thr Trp Pro Ser Pro His Lys Phe Asp Pro Asp Arg Phe Asp	380		385		390
Asp Glu Leu Val Met Lys Thr Phe Ser Ser Leu Gly Phe Ser Gly	395		400		405
Thr Gln Glu Cys Pro Glu Leu Arg Phe Ala Tyr Met Val Thr Thr	410		415		420
Val Leu Leu Ser Val Leu Val Lys Arg Leu His Leu Leu Ser Val	425		430		435

Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser
 440 445 450

Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr
 455 460

<210> 213
 <211> 759
 <212> DNA
 <213> Homo sapiens

<400> 213
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 tccagcctca gagaccgccg cccttgcccc cgagggccat gggccgggtc 100
 tcagggcttg tgccctctcg cttcctgacg ctcttgccg atctggtggt 150
 cgtcatcacc ttattctggt cccgggacag caacatacag gcctgcctgc 200
 ctctcacgtt ccccccgag gagtatgaca agcaggacat tcagctggtg 250
 gccgcgtct ctgtcacct gggcctcttt gcagtggagc tggccggttt 300
 cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350
 gggctcactg tagtgcaccc gtggccctgt ctttcttcat attcgagcgt 400
 tgggagtgca ctacgtattg gtacatcttt gtcttctgca gtgcccttcc 450
 agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500
 aacccttctg attaccttca tgacgggaac ctaaggacga agcctacagg 550
 ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcggtt 600
 ttcccctcgg aaactgcttc tgctggagga tatgtgttgg aataattacg 650
 tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaata 700
 tgttttgtag taacattaag acttatatac agttttaggg gacaattaa 750
 aaaaaaaaa 759

<210> 214
 <211> 140
 <212> PRT
 <213> Homo sapiens

<400> 214
 Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu
 1 5 10 15
 Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp
 20 25 30
 Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu
 35 40 45

Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr
 50 55 60
 Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val
 65 70 75
 Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His
 80 85 90
 Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp
 95 100 105
 Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu
 110 115 120
 Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu
 125 130 135
 Lys Lys Lys Pro Phe
 140

<210> 215
 <211> 697
 <212> DNA
 <213> Homo sapiens

<400> 215
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 cctgggctct cccagcctc cttcgactcg gagcggctca ggagacagaa 100
 gaccggcct gctgcagccc catagtcccc cggaacgagt ggaaggccct 150
 ggcacagag tgcgccagc acctgagcct gcccttacgc tatgtggtgg 200
 tatgcacac ggcgggcagc agctgcaaca ccccgccctc gtgccagcag 250
 caggcccgga atgtgcagca ctaccacatg aagacactgg gctggtgcga 300
 cgtgggctac aacttcctga ttggagaaga cgggctcgta tacgagggcc 350
 gtggctggaa cttcacgggt gccactcag gtcacttatg gaaccccatg 400
 tccattggca tcagcttcac gggcaactac atggatcggg tgcccacacc 450
 ccaggccatc cgggcagccc agggctctact ggcccgcggt gtggctcagg 500
 gagccctgag gtccaactat gtgctcaaag gacaccggga tgtgcagcgt 550
 acactctctc caggcaacca gctctaccac ctcatccaga attggccaca 600
 ctaccgctcc cctgaggcc ctgctgatcc gcacccatt cctccctcc 650
 catggccaaa aacccactg tctccttctc caataaagat gtagctc 697

<210> 216
 <211> 196
 <212> PRT

<213> Homo sapiens

<400> 216

Met Ser Arg Arg Ser Met Leu Leu Ala Trp Ala Leu Pro Ser Leu
 1 5 10 15
 Leu Arg Leu Gly Ala Ala Gln Glu Thr Glu Asp Pro Ala Cys Cys
 20 25 30
 Ser Pro Ile Val Pro Arg Asn Glu Trp Lys Ala Leu Ala Ser Glu
 35 40 45
 Cys Ala Gln His Leu Ser Leu Pro Leu Arg Tyr Val Val Val Ser
 50 55 60
 His Thr Ala Gly Ser Ser Cys Asn Thr Pro Ala Ser Cys Gln Gln
 65 70 75
 Gln Ala Arg Asn Val Gln His Tyr His Met Lys Thr Leu Gly Trp
 80 85 90
 Cys Asp Val Gly Tyr Asn Phe Leu Ile Gly Glu Asp Gly Leu Val
 95 100 105
 Tyr Glu Gly Arg Gly Trp Asn Phe Thr Gly Ala His Ser Gly His
 110 115 120
 Leu Trp Asn Pro Met Ser Ile Gly Ile Ser Phe Met Gly Asn Tyr
 125 130 135
 Met Asp Arg Val Pro Thr Pro Gln Ala Ile Arg Ala Ala Gln Gly
 140 145 150
 Leu Leu Ala Cys Gly Val Ala Gln Gly Ala Leu Arg Ser Asn Tyr
 155 160 165
 Val Leu Lys Gly His Arg Asp Val Gln Arg Thr Leu Ser Pro Gly
 170 175 180
 Asn Gln Leu Tyr His Leu Ile Gln Asn Trp Pro His Tyr Arg Ser
 185 190 195
 Pro

<210> 217

<211> 1871

<212> DNA

<213> Homo sapiens

<400> 217

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 tctatctggt catctgtggc caggatgatg gtcctcccgg ctacagaggac 150
 cctgagcgtg atgaccacga gggccagccc cggccccggg tgcctcgga 200

gcggggccac atctcaccta agtcccggcc catggccaat tccactctcc 250
tagggctgct ggccccgcct ggggaggctt ggggcattct tgggcagccc 300
cccaaccgcc cgaaccacag cccccaccc tcagccaagg tgaagaaaat 350
ctttggctgg ggcgacttct actccaacat caagacggtg gccctgaacc 400
tgctcgtcac agggaagatt gtggaccatg gcaatgggac cttcagcgtc 450
cacttccaac acaatgccac aggccaggga aacatctcca tcagcctcgt 500
gccccccagt aaagctgtag agttccacca ggaacagcag atcttcatcg 550
aagccaaggc ctccaaaatc ttcaactgcc ggatggagtg ggagaaggta 600
gaacggggcc gccggacctc gctttgcacc cagcaccag ccaagatctg 650
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tcaaagtcgt ctgtgtctac atgccttct acagcacgga ctatcggctg 750
gtccagaagg tgtgcccaga ttacaactac catagtata cccctacta 800
cccatctggg tgaccogggg caggccacag aggccaggcc agggctggaa 850
ggacaggcct gcccatgcag gagaccatct ggacaccggg caggggaagg 900
gttgggcctc aggcaggag ggggggtggag acgaggagat gccaagtggg 950
gccagggcca agtctcaagt ggcagagaaa ggtcccaag tgctgggtccc 1000
aacctgaagc tgtggagtga ctagatcaca ggagcactgg aggaggagt 1050
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ctgggtccc gaggcctgtg ggcaggccga tcagtgtggc ccagatcaa 1150
gtcatgggag gaagctaagc ccttggttct tgccatcctg aggaaagata 1200
gcaacaggga gggggagatt tcatcagtgt ggacagcctg tcaacttagg 1250
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gccagaggag ctctccagcc ctgcctagt ggcgcctga gcccttgtc 1350
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gtcttgacag attgaccatc tgtctccagc caggccacc ctttccaaaa 1450
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tgttctgtgt gtctgtctgt ggggtggggg aggggaggga agtcttgtga 1800
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aataaagctt gccccggggc a 1871

<210> 218

<211> 252

<212> PRT

<213> Homo sapiens

<400> 218

Met	Gln	Leu	Thr	Arg	Cys	Cys	Phe	Val	Phe	Leu	Val	Gln	Gly	Ser	1	5	10	15
Leu	Tyr	Leu	Val	Ile	Cys	Gly	Gln	Asp	Asp	Gly	Pro	Pro	Gly	Ser	20	25	30	
Glu	Asp	Pro	Glu	Arg	Asp	Asp	His	Glu	Gly	Gln	Pro	Arg	Pro	Arg	35	40	45	
Val	Pro	Arg	Lys	Arg	Gly	His	Ile	Ser	Pro	Lys	Ser	Arg	Pro	Met	50	55	60	
Ala	Asn	Ser	Thr	Leu	Leu	Gly	Leu	Leu	Ala	Pro	Pro	Gly	Glu	Ala	65	70	75	
Trp	Gly	Ile	Leu	Gly	Gln	Pro	Pro	Asn	Arg	Pro	Asn	His	Ser	Pro	80	85	90	
Pro	Pro	Ser	Ala	Lys	Val	Lys	Lys	Ile	Phe	Gly	Trp	Gly	Asp	Phe	95	100	105	
Tyr	Ser	Asn	Ile	Lys	Thr	Val	Ala	Leu	Asn	Leu	Leu	Val	Thr	Gly	110	115	120	
Lys	Ile	Val	Asp	His	Gly	Asn	Gly	Thr	Phe	Ser	Val	His	Phe	Gln	125	130	135	
His	Asn	Ala	Thr	Gly	Gln	Gly	Asn	Ile	Ser	Ile	Ser	Leu	Val	Pro	140	145	150	
Pro	Ser	Lys	Ala	Val	Glu	Phe	His	Gln	Glu	Gln	Gln	Ile	Phe	Ile	155	160	165	
Glu	Ala	Lys	Ala	Ser	Lys	Ile	Phe	Asn	Cys	Arg	Met	Glu	Trp	Glu	170	175	180	
Lys	Val	Glu	Arg	Gly	Arg	Arg	Thr	Ser	Leu	Cys	Thr	His	Asp	Pro	185	190	195	
Ala	Lys	Ile	Cys	Ser	Arg	Asp	His	Ala	Gln	Ser	Ser	Ala	Thr	Trp	200	205	210	

Gly	Ile	Ser	Val	Arg	Ala	Ala	Asn	Ser	Lys	Val	Ala	Phe	Ser	Ala	
				65					70					75	
Val	Arg	Ser	Thr	Asn	His	Glu	Pro	Ser	Glu	Met	Ser	Asn	Lys	Thr	
				80					85					90	
Arg	Ile	Ile	Tyr	Phe	Asp	Gln	Ile	Leu	Val	Asn	Val	Gly	Asn	Phe	
				95					100					105	
Phe	Thr	Leu	Glu	Ser	Val	Phe	Val	Ala	Pro	Arg	Lys	Gly	Ile	Tyr	
				110					115					120	
Ser	Phe	Ser	Phe	His	Val	Ile	Lys	Val	Tyr	Gln	Ser	Gln	Thr	Ile	
				125					130					135	
Gln	Val	Asn	Leu	Met	Leu	Asn	Gly	Lys	Pro	Val	Ile	Ser	Ala	Phe	
				140					145					150	
Ala	Gly	Asp	Lys	Asp	Val	Thr	Arg	Glu	Ala	Ala	Thr	Asn	Gly	Val	
				155					160					165	
Leu	Leu	Tyr	Leu	Asp	Lys	Glu	Asp	Lys	Val	Tyr	Leu	Lys	Leu	Glu	
				170					175					180	
Lys	Gly	Asn	Leu	Val	Gly	Gly	Trp	Gln	Tyr	Ser	Thr	Phe	Ser	Gly	
				185					190					195	
Phe	Leu	Val	Phe	Pro	Leu										
				200											

<210> 221
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 221
 acggctcacc atgggctccg 20

<210> 222
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 222
 aggaagagga gcccttggag tccg 24

<210> 223
 <211> 40

<213> Homo sapiens

<400> 225

Met Thr Ala Ala Val Phe Phe Gly Cys Ala Phe Ile Ala Phe Gly
1 5 10 15

Pro Ala Leu Ala Leu Tyr Val Phe Thr Ile Ala Ile Glu Pro Leu
20 25 30

Arg Ile Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val Ser
35 40 45

Leu Leu Ile Ser Ser Leu Val Trp Phe Met Ala Arg Val Ile Ile
50 55 60

Asp Asn Lys Asp Gly Pro Thr Gln Lys Tyr Leu Leu Ile Phe Gly
65 70 75

Ala Phe Val Ser Val Tyr Ile Gln Glu Met Phe Arg Phe Ala Tyr
80 85 90

Tyr Lys Leu Leu Lys Lys Ala Ser Glu Gly Leu Lys Ser Ile Asn
95 100 105

Pro Gly Glu Thr Ala Pro Ser Met Arg Leu Leu Ala Tyr Val Ser
110 115 120

Gly Leu Gly Phe Gly Ile Met Ser Gly Val Phe Ser Phe Val Asn
125 130 135

Thr Leu Ser Asp Ser Leu Gly Pro Gly Thr Val Gly Ile His Gly
140 145 150

Asp Ser Pro Gln Phe Phe Leu Tyr Ser Ala Phe Met Thr Leu Val
155 160 165

Ile Ile Leu Leu His Val Phe Trp Gly Ile Val Phe Phe Asp Gly
170 175 180

Cys Glu Lys Lys Lys Trp Gly Ile Leu Leu Ile Val Leu Leu Thr
185 190 195

His Leu Leu Val Ser Ala Gln Thr Phe Ile Ser Ser Tyr Tyr Gly
200 205 210

Ile Asn Leu Ala Ser Ala Phe Ile Ile Leu Val Leu Met Gly Thr
215 220 225

Trp Ala Phe Leu Ala Ala Gly Gly Ser Cys Arg Ser Leu Lys Leu
230 235 240

Cys Leu Leu Cys Gln Asp Lys Asn Phe Leu Leu Tyr Asn Gln Arg
245 250 255

Ser Arg

<210> 226

<211> 3939
<212> DNA
<213> Homo sapiens

<400> 226

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agtttgagcg cacctacgtg gacgaggtca acagcgagct ggtcaacatc 200
tacaccttca accatactgt gacccgcaac aggacagagg gcgtgcgtgt 250
gtctgtgaac gtctgaaca agcagaaggg ggcccgcttg ctgtttgttg 300
tccgccagaa ggaggctgtg gtgtccttcc aggtgcccct aatcctgcga 350
gggatgtttc agcgcaagta cctctaccaa aaagtgaac gaaccctgtg 400
tcagccccc accaagaatg agtcggagat tcagttcttc tacgtggatg 450
tgtccacct gtcaccagtc aacaccacat accagctccg ggtcagccgc 500
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 aacaacatcc tcagcaacct ggggtacatc ctgctggggc tgcttttct 1600
 gctcatcatc ctgcaacggg agatcaacca caaccgggccc ctgctgcgca 1650
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 tcgctggctg cctatgggct tatcatgcgc ccaatgatt tcgcttctta 2200
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<211> 832

<212> PRT

<213> Homo sapiens

<400> 227

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20 25 30

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Ile Asp Arg Ala Cys Pro Glu Ser Gly	His Pro Arg Val Leu Ala	
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Asp Ser Phe Pro Gly Ser Ser Pro Tyr	Glu Gly Tyr Asn Tyr Gly	
350	355	360
Ser Phe Glu Asn Val Ser Gly Ser Thr	Asp Gly Leu Val Asp Ser	
365	370	375
Ala Gly Thr Gly Asp Leu Ser Tyr Gly	Tyr Gln Gly Arg Ser Phe	
380	385	390
Glu Pro Val Gly Thr Arg Pro Arg Val	Asp Ser Met Ser Ser Val	
395	400	405
Glu Glu Asp Asp Tyr Asp Thr Leu Thr	Asp Ile Asp Ser Asp Lys	
410	415	420
Asn Val Ile Arg Thr Lys Gln Tyr Leu	Tyr Val Ala Asp Leu Ala	
425	430	435
Arg Lys Asp Lys Arg Val Leu Arg Lys	Lys Tyr Gln Ile Tyr Phe	
440	445	450
Trp Asn Ile Ala Thr Ile Ala Val Phe	Tyr Ala Leu Pro Val Val	
455	460	465
Gln Leu Val Ile Thr Tyr Gln Thr Val	Val Asn Val Thr Gly Asn	
470	475	480
Gln Asp Ile Cys Tyr Tyr Asn Phe Leu	Cys Ala His Pro Leu Gly	
485	490	495
Asn Leu Ser Ala Phe Asn Asn Ile Leu	Ser Asn Leu Gly Tyr Ile	
500	505	510
Leu Leu Gly Leu Leu Phe Leu Leu Ile	Ile Leu Gln Arg Glu Ile	
515	520	525
Asn His Asn Arg Ala Leu Leu Arg Asn	Asp Leu Cys Ala Leu Glu	
530	535	540
Cys Gly Ile Pro Lys His Phe Gly Leu	Phe Tyr Ala Met Gly Thr	
545	550	555
Ala Leu Met Met Glu Gly Leu Leu Ser	Ala Cys Tyr His Val Cys	
560	565	570
Pro Asn Tyr Thr Asn Phe Gln Phe Asp	Thr Ser Phe Met Tyr Met	
575	580	585
Ile Ala Gly Leu Cys Met Leu Lys Leu	Tyr Gln Lys Arg His Pro	
590	595	600
Asp Ile Asn Ala Ser Ala Tyr Ser Ala	Tyr Ala Cys Leu Ala Ile	
605	610	615

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Leu	Pro	Arg	Glu	Gly	Ala	Glu	Gly	Gln	Ile	Val	Leu	Ser	Gly	Asp
				50					55					60
Ser	Gly	Lys	Ala	Thr	Glu	Gly	Pro	Phe	Ala	Met	Asp	Pro	Asp	Ser
				65					70					75
Gly	Phe	Leu	Leu	Val	Thr	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Gln	Ala
				80					85					90
Glu	Tyr	Gln	Leu	Gln	Val	Thr	Leu	Glu	Met	Gln	Asp	Gly	His	Val
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Leu	Trp	Gly	Pro	Gln	Pro	Val	Leu	Val	His	Val	Lys	Asp	Glu	Asn
				110					115					120
Asp	Gln	Val	Pro	His	Phe	Ser	Gln	Ala	Ile	Tyr	Arg	Ala	Arg	Leu
				125					130					135
Ser	Arg	Gly	Thr	Arg	Pro	Gly	Ile	Pro	Phe	Leu	Phe	Leu	Glu	Ala
				140					145					150
Ser	Asp	Arg	Asp	Glu	Pro	Gly	Thr	Ala	Asn	Ser	Asp	Leu	Arg	Phe
				155					160					165
His	Ile	Leu	Ser	Gln	Ala	Pro	Ala	Gln	Pro	Ser	Pro	Asp	Met	Phe
				170					175					180
Gln	Leu	Glu	Pro	Arg	Leu	Gly	Ala	Leu	Ala	Leu	Ser	Pro	Lys	Gly
				185					190					195
Ser	Thr	Ser	Leu	Asp	His	Ala	Leu	Glu	Arg	Thr	Tyr	Gln	Leu	Leu
				200					205					210
Val	Gln	Val	Lys	Asp	Met	Gly	Asp	Gln	Ala	Ser	Gly	His	Gln	Ala
				215					220					225
Thr	Ala	Thr	Val	Glu	Val	Ser	Ile	Ile	Glu	Ser	Thr	Trp	Val	Ser
				230					235					240
Leu	Glu	Pro	Ile	His	Leu	Ala	Glu	Asn	Leu	Lys	Val	Leu	Tyr	Pro
				245					250					255
His	His	Met	Ala	Gln	Val	His	Trp	Ser	Gly	Gly	Asp	Val	His	Tyr
				260					265					270
His	Leu	Glu	Ser	His	Pro	Pro	Gly	Pro	Phe	Glu	Val	Asn	Ala	Glu
				275					280					285
Gly	Asn	Leu	Tyr	Val	Thr	Arg	Glu	Leu	Asp	Arg	Glu	Ala	Gln	Ala
				290					295					300
Glu	Tyr	Leu	Leu	Gln	Val	Arg	Ala	Gln	Asn	Ser	His	Gly	Glu	Asp
				305					310					315

Tyr	Ala	Ala	Pro	Leu	Glu	Leu	His	Val	Leu	Val	Met	Asp	Glu	Asn	
				320					325					330	
Asp	Asn	Val	Pro	Ile	Cys	Pro	Pro	Arg	Asp	Pro	Thr	Val	Ser	Ile	
				335					340					345	
Pro	Glu	Leu	Ser	Pro	Pro	Gly	Thr	Glu	Val	Thr	Arg	Leu	Ser	Ala	
				350					355					360	
Glu	Asp	Ala	Asp	Ala	Pro	Gly	Ser	Pro	Asn	Ser	His	Val	Val	Tyr	
				365					370					375	
Gln	Leu	Leu	Ser	Pro	Glu	Pro	Glu	Asp	Gly	Val	Glu	Gly	Arg	Ala	
				380					385					390	
Phe	Gln	Val	Asp	Pro	Thr	Ser	Gly	Ser	Val	Thr	Leu	Gly	Val	Leu	
				395					400					405	
Pro	Leu	Arg	Ala	Gly	Gln	Asn	Ile	Leu	Leu	Leu	Val	Leu	Ala	Met	
				410					415					420	
Asp	Leu	Ala	Gly	Ala	Glu	Gly	Gly	Phe	Ser	Ser	Thr	Cys	Glu	Val	
				425					430					435	
Glu	Val	Ala	Val	Thr	Asp	Ile	Asn	Asp	His	Ala	Pro	Glu	Phe	Ile	
				440					445					450	
Thr	Ser	Gln	Ile	Gly	Pro	Ile	Ser	Leu	Pro	Glu	Asp	Val	Glu	Pro	
				455					460					465	
Gly	Thr	Leu	Val	Ala	Met	Leu	Thr	Ala	Ile	Asp	Ala	Asp	Leu	Glu	
				470					475					480	
Pro	Ala	Phe	Arg	Leu	Met	Asp	Phe	Ala	Ile	Glu	Arg	Gly	Asp	Thr	
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Glu	Gly	Thr	Phe	Gly	Leu	Asp	Trp	Glu	Pro	Asp	Ser	Gly	His	Val	
				500					505					510	
Arg	Leu	Arg	Leu	Cys	Lys	Asn	Leu	Ser	Tyr	Glu	Ala	Ala	Pro	Ser	
				515					520					525	
His	Glu	Val	Val	Val	Val	Val	Gln	Ser	Val	Ala	Lys	Leu	Val	Gly	
				530					535					540	
Pro	Gly	Pro	Gly	Pro	Gly	Ala	Thr	Ala	Thr	Val	Thr	Val	Leu	Val	
				545					550					555	
Glu	Arg	Val	Met	Pro	Pro	Pro	Lys	Leu	Asp	Gln	Glu	Ser	Tyr	Glu	
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Ala	Ser	Val	Pro	Ile	Ser	Ala	Pro	Ala	Gly	Ser	Phe	Leu	Leu	Thr	
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Ile	Gln	Pro	Ser	Asp	Pro	Ile	Ser	Arg	Thr	Leu	Arg	Phe	Ser	Leu	
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Val	Asn	Asp	Ser	Glu	Gly	Trp	Leu	Cys	Ile	Glu	Lys	Phe	Ser	Gly	

				605					610					615
Glu	Val	His	Thr	Ala 620	Gln	Ser	Leu	Gln	Gly 625	Ala	Gln	Pro	Gly	Asp 630
Thr	Tyr	Thr	Val	Leu 635	Val	Glu	Ala	Gln	Asp 640	Thr	Ala	Leu	Thr	Leu 645
Ala	Pro	Val	Pro	Ser 650	Gln	Tyr	Leu	Cys	Thr 655	Pro	Arg	Gln	Asp	His 660
Gly	Leu	Ile	Val	Ser 665	Gly	Pro	Ser	Lys	Asp 670	Pro	Asp	Leu	Ala	Ser 675
Gly	His	Gly	Pro	Tyr 680	Ser	Phe	Thr	Leu	Gly 685	Pro	Asn	Pro	Thr	Val 690
Gln	Arg	Asp	Trp	Arg 695	Leu	Gln	Thr	Leu	Asn 700	Gly	Ser	His	Ala	Tyr 705
Leu	Thr	Leu	Ala	Leu 710	His	Trp	Val	Glu	Pro 715	Arg	Glu	His	Ile	Ile 720
Pro	Val	Val	Val	Ser 725	His	Asn	Ala	Gln	Met 730	Trp	Gln	Leu	Leu	Val 735
Arg	Val	Ile	Val	Cys 740	Arg	Cys	Asn	Val	Glu 745	Gly	Gln	Cys	Met	Arg 750
Lys	Val	Gly	Arg	Met 755	Lys	Gly	Met	Pro	Thr 760	Lys	Leu	Ser	Ala	Val 765
Gly	Ile	Leu	Val	Gly 770	Thr	Leu	Val	Ala	Ile 775	Gly	Ile	Phe	Leu	Ile 780
Leu	Ile	Phe	Thr	His 785	Trp	Thr	Met	Ser	Arg 790	Lys	Lys	Asp	Pro	Asp 795
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<220>
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<222> 1-50
<223> Synthetic construct.

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<211> 24
<212> DNA
<213> Artificial Sequeunce
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<220>
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 <222> full
 <223> Synthetic oligonucleotide probe

<400> 231
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<210> 232
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 232
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<210> 233
 <211> 2786
 <212> DNA
 <213> Homo sapiens

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 acttgaagct caatttcttg aaatctccct cctccttcaa tcggcctgtg 200
 gatgtcctgg tcccatctgt cagtctgcag gcattttaa ccttctctgag 250
 atcccagggc ttagagtacg cagtgacaat tgaggacctg caggcccttt 300
 tagacaatga agatgatgaa atgcaacaca atgaagggca agaacggagc 350
 agtaataact tcaactacgg ggcttaccat tccctggaag ctattttacca 400
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<400> 235

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 aacaccgact ttgccttccg cctataccgc aggctgggtt tggagacccc 250
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 <211> 417
 <212> PRT
 <213> Homo sapiens

<400> 236
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 Pro Arg Pro Ser Ser Thr Lys Ser Thr Pro Ala Ser Gln Val Tyr
 35 40 45
 Ser Leu Asn Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val
 50 55 60
 Leu Glu Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val
 65 70 75
 Ser Thr Ser Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr
 80 85 90
 Lys Thr Gln Ile Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr
 95 100 105
 Pro Glu Ser Ala Ile His Gln Gly Phe Gln His Leu Val His Ser
 110 115 120
 Leu Thr Val Pro Ser Lys Asp Leu Thr Leu Lys Met Gly Ser Ala
 125 130 135
 Leu Phe Val Lys Lys Glu Leu Gln Leu Gln Ala Asn Phe Leu Gly
 140 145 150
 Asn Val Lys Arg Leu Tyr Glu Ala Glu Val Phe Ser Thr Asp Phe
 155 160 165
 Ser Asn Pro Ser Ile Ala Gln Ala Arg Ile Asn Ser His Val Lys
 170 175 180
 Lys Lys Thr Gln Gly Lys Val Val Asp Ile Ile Gln Gly Leu Asp
 185 190 195
 Leu Leu Thr Ala Met Val Leu Val Asn His Ile Phe Phe Lys Ala

200	205	210
Lys Trp Glu Lys Pro Phe His Leu Glu Tyr Thr Arg Lys Asn Phe 215	220	225
Pro Phe Leu Val Gly Glu Gln Val Thr Val Gln Val Pro Met Met 230	235	240
His Gln Lys Glu Gln Phe Ala Phe Gly Val Asp Thr Glu Leu Asn 245	250	255
Cys Phe Val Leu Gln Met Asp Tyr Lys Gly Asp Ala Val Ala Phe 260	265	270
Phe Val Leu Pro Ser Lys Gly Lys Met Arg Gln Leu Glu Gln Ala 275	280	285
Leu Ser Ala Arg Thr Leu Ile Lys Trp Ser His Ser Leu Gln Lys 290	295	300
Arg Trp Ile Glu Val Phe Ile Pro Arg Phe Ser Ile Ser Ala Ser 305	310	315
Tyr Asn Leu Glu Thr Ile Leu Pro Lys Met Gly Ile Gln Asn Ala 320	325	330
Phe Asp Lys Asn Ala Asp Phe Ser Gly Ile Ala Lys Arg Asp Ser 335	340	345
Leu Gln Val Ser Lys Ala Thr His Lys Ala Val Leu Asp Val Ser 350	355	360
Glu Glu Gly Thr Glu Ala Thr Ala Ala Thr Thr Thr Lys Phe Ile 365	370	375
Val Arg Ser Lys Asp Gly Pro Ser Tyr Phe Thr Val Ser Phe Asn 380	385	390
Arg Thr Phe Leu Met Met Ile Thr Asn Lys Ala Thr Asp Gly Ile 395	400	405
Leu Phe Leu Gly Lys Val Glu Asn Pro Thr Lys Ser 410	415	

<210> 237

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 237

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<210> 238

<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 238
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<210> 239
<211> 24
<212> DNA
<213> Artificial

<220>
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<222> 1-24
<223> Synthetic construct.

<400> 239
tgactcgggg tctccaaaac cagc 24

<210> 240
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 240
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<210> 241
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 241
ggcatcttac ctttatggag tactctttgc tgttggcctc tgtgctcc 48

<210> 242
<211> 2436
<212> DNA
<213> Homo sapiens

<400> 242
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Thr	Asn	Ser	Glu	Ser 110	Ser	Thr	Thr	Ser	Ser 115	Gly	Ala	Ser	Thr	Ala 120
Thr	Asn	Ser	Glu	Ser 125	Ser	Thr	Pro	Ser	Ser 130	Gly	Ala	Ser	Thr	Val 135
Thr	Asn	Ser	Gly	Ser 140	Ser	Val	Thr	Ser	Ser 145	Gly	Ala	Ser	Thr	Ala 150
Thr	Asn	Ser	Glu	Ser 155	Ser	Thr	Val	Ser	Ser 160	Arg	Ala	Ser	Thr	Ala 165
Thr	Asn	Ser	Glu	Ser 170	Ser	Thr	Leu	Ser	Ser 175	Gly	Ala	Ser	Thr	Ala 180
Thr	Asn	Ser	Asp	Ser 185	Ser	Thr	Thr	Ser	Ser 190	Gly	Ala	Ser	Thr	Ala 195
Thr	Asn	Ser	Glu	Ser 200	Ser	Thr	Thr	Ser	Ser 205	Gly	Ala	Ser	Thr	Ala 210
Thr	Asn	Ser	Glu	Ser 215	Ser	Thr	Val	Ser	Ser 220	Arg	Ala	Ser	Thr	Ala 225
Thr	Asn	Ser	Glu	Ser 230	Ser	Thr	Thr	Ser	Ser 235	Gly	Ala	Ser	Thr	Ala 240
Thr	Asn	Ser	Glu	Ser 245	Arg	Thr	Thr	Ser	Asn 250	Gly	Ala	Gly	Thr	Ala 255
Thr	Asn	Ser	Glu	Ser 260	Ser	Thr	Thr	Ser	Ser 265	Gly	Ala	Ser	Thr	Ala 270
Thr	Asn	Ser	Asp	Ser 275	Ser	Thr	Val	Ser	Ser 280	Gly	Ala	Ser	Thr	Ala 285
Thr	Asn	Ser	Glu	Ser 290	Ser	Thr	Thr	Ser	Ser 295	Gly	Ala	Ser	Thr	Ala 300
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Thr	Asn	Ser	Glu	Ser 335	Ser	Thr	Val	Ser	Ser 340	Gly	Ile	Ser	Thr	Val 345
Thr	Asn	Ser	Glu	Ser 350	Ser	Thr	Pro	Ser	Ser 355	Gly	Ala	Asn	Thr	Ala 360
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala

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395		400	405
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala			
410		415	420
Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Glu Ala Ser Thr Ala			
425		430	435
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val			
440		445	450
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala			
455		460	465
Thr Asn Ser Gly Ser Ser Val Thr Ser Ala Gly Ser Gly Thr Ala			
470		475	480
Ala Leu Thr Gly Met His Thr Thr Ser His Ser Ala Ser Thr Ala			
485		490	495
Val Ser Glu Ala Lys Pro Gly Gly Ser Leu Val Pro Trp Glu Ile			
500		505	510
Phe Leu Ile Thr Leu Val Ser Val Val Ala Ala Val Gly Leu Phe			
515		520	525
Ala Gly Leu Phe Phe Cys Val Arg Asn Ser Leu Ser Leu Arg Asn			
530		535	540
Thr Phe Asn Thr Ala Val Tyr His Pro His Gly Leu Asn His Gly			
545		550	555
Leu Gly Pro Gly Pro Gly Gly Asn His Gly Ala Pro His Arg Pro			
560		565	570
Arg Trp Ser Pro Asn Trp Phe Trp Arg Arg Pro Val Ser Ser Ile			
575		580	585
Ala Met Glu Met Ser Gly Arg Asn Ser Gly Pro			
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<210> 244

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 244

<400> 252

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Gln	Glu	Leu	Leu	Trp 110	Gly	Ala	Asp	Ala	Glu 115	Lys	Lys	Gln	Gln	Cys 120
Ser	Phe	Lys	Gly	Lys 125	Asp	Pro	Gln	Arg	Asp 130	Cys	Gln	Asn	Tyr	Ile 135
Lys	Ile	Leu	Leu	Pro 140	Leu	Ser	Gly	Ser	His 145	Leu	Phe	Thr	Cys	Gly 150
Thr	Ala	Ala	Phe	Ser 155	Pro	Met	Cys	Thr	Tyr 160	Ile	Asn	Met	Glu	Asn 165
Phe	Thr	Leu	Ala	Arg 170	Asp	Glu	Lys	Gly	Asn 175	Val	Leu	Leu	Glu	Asp 180
Gly	Lys	Gly	Arg	Cys 185	Pro	Phe	Asp	Pro	Asn 190	Phe	Lys	Ser	Thr	Ala 195
Leu	Val	Val	Asp	Gly 200	Glu	Leu	Tyr	Thr	Gly 205	Thr	Val	Ser	Ser	Phe 210
Gln	Gly	Asn	Asp	Pro 215	Ala	Ile	Ser	Arg	Ser 220	Gln	Ser	Leu	Arg	Pro 225
Thr	Lys	Thr	Glu	Ser 230	Ser	Leu	Asn	Trp	Leu 235	Gln	Asp	Pro	Ala	Phe 240
Val	Ala	Ser	Ala	Tyr 245	Ile	Pro	Glu	Ser	Leu 250	Gly	Ser	Leu	Gln	Gly 255
Asp	Asp	Asp	Lys	Ile 260	Tyr	Phe	Phe	Phe	Ser 265	Glu	Thr	Gly	Gln	Glu 270
Phe	Glu	Phe	Phe	Glu 275	Asn	Thr	Ile	Val	Ser 280	Arg	Ile	Ala	Arg	Ile 285
Cys	Lys	Gly	Asp	Glu 290	Gly	Gly	Glu	Arg	Val 295	Leu	Gln	Gln	Arg	Trp 300
Thr	Ser	Phe	Leu	Lys 305	Ala	Gln	Leu	Leu	Cys 310	Ser	Arg	Pro	Asp	Asp 315
Gly	Phe	Pro	Phe	Asn 320	Val	Leu	Gln	Asp	Val 325	Phe	Thr	Leu	Ser	Pro 330
Ser	Pro	Gln	Asp	Trp 335	Arg	Asp	Thr	Leu	Phe 340	Tyr	Gly	Val	Phe	Thr 345
Ser	Gln	Trp	His	Arg 350	Gly	Thr	Thr	Glu	Gly 355	Ser	Ala	Val	Cys	Val 360
Phe	Thr	Met	Lys	Asp 365	Val	Gln	Arg	Val	Phe 370	Ser	Gly	Leu	Tyr	Lys 375

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Glu	Asp	Gly	Val	Ala 680	Asp	Gln	Thr	Asp	Glu 685	Gly	Gly	Ser	Val	Pro 690
Val	Ile	Ile	Ser	Thr 695	Ser	Arg	Val	Ser	Ala 700	Pro	Ala	Gly	Gly	Lys 705
Ala	Ser	Trp	Gly	Ala 710	Asp	Arg	Ser	Tyr	Trp 715	Lys	Glu	Phe	Leu	Val 720
Met	Cys	Thr	Leu	Phe 725	Val	Leu	Ala	Val	Leu 730	Leu	Pro	Val	Leu	Phe 735
Leu	Leu	Tyr	Arg	His 740	Arg	Asn	Ser	Met	Lys 745	Val	Phe	Leu	Lys	Gln 750
Gly	Glu	Cys	Ala	Ser 755	Val	His	Pro	Lys	Thr 760	Cys	Pro	Val	Val	Leu 765
Pro	Pro	Glu	Thr	Arg 770	Pro	Leu	Asn	Gly	Leu 775	Gly	Pro	Pro	Ser	Thr 780
Pro	Leu	Asp	His	Arg 785	Gly	Tyr	Gln	Ser	Leu 790	Ser	Asp	Ser	Pro	Pro 795
Gly	Ala	Arg	Val	Phe 800	Thr	Glu	Ser	Glu	Lys 805	Arg	Pro	Leu	Ser	Ile 810
Gln	Asp	Ser	Phe	Val 815	Glu	Val	Ser	Pro	Val 820	Cys	Pro	Arg	Pro	Arg 825
Val	Arg	Leu	Gly	Ser 830	Glu	Ile	Arg	Asp	Ser 835	Val	Val			

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<210> 254
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 254
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<210> 255
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.
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Lys Cys Leu Arg	Glu Met Tyr Thr Thr	His Glu Asp Val Glu Val	245	250	255
Gly Arg Cys Val	Arg Arg Phe Ala Gly	Val Gln Cys Val Trp Ser	260	265	270
Tyr Glu Met Arg	Gln Leu Phe Tyr Glu	Asn Tyr Glu Gln Asn Lys	275	280	285
Lys Gly Tyr Ile	Arg Asp Leu His Asn	Ser Lys Ile His Gln Ala	290	295	300
Ile Thr Leu His	Pro Asn Lys Asn Pro	Pro Tyr Gln Tyr Arg Leu	305	310	315
His Ser Tyr Met	Leu Ser Arg Lys Ile	Ser Glu Leu Arg His Arg	320	325	330
Thr Ile Gln Leu	His Arg Glu Ile Val	Leu Met Ser Lys Tyr Ser	335	340	345
Asn Thr Glu Ile	His Lys Glu Asp Leu	Gln Leu Gly Ile Pro Pro	350	355	360
Ser Phe Met Arg	Phe Gln Pro Arg Gln	Arg Glu Glu Ile Leu Glu	365	370	375
Trp Glu Phe Leu	Thr Gly Lys Tyr Leu	Tyr Ser Ala Val Asp Gly	380	385	390
Gln Pro Pro Arg	Arg Gly Met Asp Ser	Ala Gln Arg Glu Ala Leu	395	400	405
Asp Asp Ile Val	Met Gln Val Met Glu	Met Ile Asn Ala Asn Ala	410	415	420
Lys Thr Arg Gly	Arg Ile Ile Asp Phe	Lys Glu Ile Gln Tyr Gly	425	430	435
Tyr Arg Arg Val	Asn Pro Met Tyr Gly	Ala Glu Tyr Ile Leu Asp	440	445	450
Leu Leu Leu Leu	Tyr Lys Lys His Lys	Gly Lys Lys Met Thr Val	455	460	465
Pro Val Arg Arg	His Ala Tyr Leu Gln	Gln Thr Phe Ser Lys Ile	470	475	480
Gln Phe Val Glu	His Glu Glu Leu Asp	Ala Gln Glu Leu Ala Lys	485	490	495
Arg Ile Asn Gln	Glu Ser Gly Ser Leu	Ser Phe Leu Ser Asn Ser	500	505	510
Leu Lys Lys Leu	Val Pro Phe Gln Leu	Pro Gly Ser Lys Ser Glu	515	520	525
His Lys Glu Pro	Lys Asp Lys Lys Ile	Asn Ile Leu Ile Pro Leu			

530	535	540
Ser Gly Arg Phe Asp Met Phe Val Arg	Phe Met Gly Asn Phe Glu	
545	550	555
Lys Thr Cys Leu Ile Pro Asn Gln Asn	Val Lys Leu Val Val Leu	
560	565	570
Leu Phe Asn Ser Asp Ser Asn Pro Asp	Lys Ala Lys Gln Val Glu	
575	580	585
Leu Met Arg Asp Tyr Arg Ile Lys Tyr	Pro Lys Ala Asp Met Gln	
590	595	600
Ile Leu Pro Val Ser Gly Glu Phe Ser	Arg Ala Leu Ala Leu Glu	
605	610	615
Val Gly Ser Ser Gln Phe Asn Asn Glu	Ser Leu Leu Phe Phe Cys	
620	625	630
Asp Val Asp Leu Val Phe Thr Thr Glu	Phe Leu Gln Arg Cys Arg	
635	640	645
Ala Asn Thr Val Leu Gly Gln Gln Ile	Tyr Phe Pro Ile Ile Phe	
650	655	660
Ser Gln Tyr Asp Pro Lys Ile Val Tyr	Ser Gly Lys Val Pro Ser	
665	670	675
Asp Asn His Phe Ala Phe Thr Gln Lys	Thr Gly Phe Trp Arg Asn	
680	685	690
Tyr Gly Phe Gly Ile Thr Cys Ile Tyr	Lys Gly Asp Leu Val Arg	
695	700	705
Val Gly Gly Phe Asp Val Ser Ile Gln	Gly Trp Gly Leu Glu Asp	
710	715	720
Val Asp Leu Phe Asn Lys Val Val Gln	Ala Gly Leu Lys Thr Phe	
725	730	735
Arg Ser Gln Glu Val Gly Val Val His	Val His His Pro Val Phe	
740	745	750
Cys Asp Pro Asn Leu Asp Pro Lys Gln	Tyr Lys Met Cys Leu Gly	
755	760	765
Ser Lys Ala Ser Thr Tyr Gly Ser Thr	Gln Gln Leu Ala Glu Met	
770	775	780
Trp Leu Glu Lys Asn Asp Pro Ser Tyr	Ser Lys Ser Ser Asn Asn	
785	790	795
Asn Gly Ser Val Arg Thr Ala		
800		

<210> 261
<211> 24

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	65		70		75
Glu Leu Val Thr	80	His Gly Asp Ala Ser	85	Thr Glu Asn Asp Val Leu	90
Thr Asn Pro Ile	95	Ser Glu Glu Thr Thr	100	Thr Phe Pro Thr Gly Gly	105
Phe Thr Pro Glu	110	Ile Gly Lys Lys Lys	115	His Thr Glu Ser Thr Pro	120
Phe Trp Ser Ile	125	Lys Pro Asn Asn Val	130	Ser Ile Val Leu His Ala	135
Glu Glu Pro Tyr	140	Ile Glu Asn Glu Glu	145	Pro Glu Pro Glu Pro Glu	150
Pro Ala Ala Lys	155	Gln Thr Glu Ala Pro	160	Arg Met Leu Pro Val Val	165
Thr Glu Ser Ser	170	Thr Ser Pro Tyr Val	175	Thr Ser Tyr Lys Ser Pro	180
Val Thr Thr Leu	185	Asp Lys Ser Thr Gly	190	Ile Glu Ile Ser Thr Glu	195
Ser Glu Asp Val	200	Pro Gln Leu Ser Gly	205	Glu Thr Ala Ile Glu Lys	210
Pro Glu Glu Phe	215	Gly Lys His Pro Glu	220	Ser Trp Asn Asn Asp Asp	225
Ile Leu Lys Lys	230	Ile Leu Asp Ile Asn	235	Ser Gln Val Gln Gln Ala	240
Leu Leu Ser Asp	245	Thr Ser Asn Pro Ala	250	Tyr Arg Glu Asp Ile Glu	255
Ala Ser Lys Asp	260	His Leu Lys Arg Ser	265	Leu Ala Leu Ala Ala Ala	270
Ala Glu His Lys	275	Leu Lys Thr Met Tyr	280	Lys Ser Gln Leu Leu Pro	285
Val Gly Arg Thr	290	Ser Asn Lys Ile Asp	295	Asp Ile Glu Thr Val Ile	300
Asn Met Leu Cys	305	Asn Ser Arg Ser Lys	310	Leu Tyr Glu Tyr Leu Asp	315
Ile Lys Cys Val	320	Pro Pro Glu Met Arg	325	Glu Lys Ala Ala Thr Val	330
Phe Asn Thr Leu	335	Lys Asn Met Cys Arg	340	Ser Arg Arg Val Thr Ala	345

Leu Leu Lys Val Tyr
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<210> 266
<211> 2403
<212> DNA
<213> Homo sapiens

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ttcatagtgt gagatcaacc cacaggaata tccatggctt ttgtgctcat 150
tttggttctc agtttctacg agctggtgtc aggacagtgg caagtcaactg 200
gaccgggcaa gtttgtccag gccttgggtg gggaggacgc cgtgttctcc 250
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ctcggacatc ggctgtatg ggtgctggtt cagttcccag atttacgatg 500
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tcacaggtga	agattaaaga	gacaacgaat	gtgaatcatg	cttgcaaggt	1950
tgagggcaca	gtgtttgcta	atgatgtgtt	tttatattat	acattttccc	2000
accataaact	ctgtttgctt	attccacatt	aatttacttt	tctctatacc	2050
aatcaccca	tggaatagtt	attgaacacc	tgctttgtga	ggctcaaaga	2100
ataaagagga	ggtaggattt	ttcactgatt	ctataagccc	agcattacct	2150
gataccaaaa	ccaggcaaag	aaaacagaag	aagaggaagg	aaaactacag	2200
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<210> 267

<211> 466

<212> PRT

<213> Homo sapiens

<400> 267

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35	40	45
Thr Ser Ala Glu Ala	Met Glu Val Arg Phe	Phe Arg Asn Gln Phe
50	55	60
His Ala Val Val His	Leu Tyr Arg Asp Gly	Glu Asp Trp Glu Ser
65	70	75
Lys Gln Met Pro Gln	Tyr Arg Gly Arg Thr	Glu Phe Val Lys Asp
80	85	90
Ser Ile Ala Gly Gly	Arg Val Ser Leu Arg	Leu Lys Asn Ile Thr
95	100	105
Pro Ser Asp Ile Gly	Leu Tyr Gly Cys Trp	Phe Ser Ser Gln Ile
110	115	120
Tyr Asp Glu Glu Ala	Thr Trp Glu Leu Arg	Val Ala Ala Leu Gly
125	130	135
Ser Leu Pro Leu Ile	Ser Ile Val Gly Tyr	Val Asp Gly Gly Ile
140	145	150
Gln Leu Leu Cys Leu	Ser Ser Gly Trp Phe	Pro Gln Pro Thr Ala
155	160	165
Lys Trp Lys Gly Pro	Gln Gly Gln Asp Leu	Ser Ser Asp Ser Arg
170	175	180
Ala Asn Ala Asp Gly	Tyr Ser Leu Tyr Asp	Val Glu Ile Ser Ile
185	190	195
Ile Val Gln Glu Asn	Ala Gly Ser Ile Leu	Cys Ser Ile His Leu
200	205	210
Ala Glu Gln Ser His	Glu Val Glu Ser Lys	Val Leu Ile Gly Glu
215	220	225
Thr Phe Phe Gln Pro	Ser Pro Trp Arg Leu	Ala Ser Ile Leu Leu
230	235	240
Gly Leu Leu Cys Gly	Ala Leu Cys Gly Val	Val Met Gly Met Ile
245	250	255
Ile Val Phe Phe Lys	Ser Lys Gly Lys Ile	Gln Ala Glu Leu Asp
260	265	270
Trp Arg Arg Lys His	Gly Gln Ala Glu Leu	Arg Asp Ala Arg Lys
275	280	285
His Ala Val Glu Val	Thr Leu Asp Pro Glu	Thr Ala His Pro Lys
290	295	300
Leu Cys Val Ser Asp	Leu Lys Thr Val Thr	His Arg Lys Ala Pro
305	310	315

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<210> 269
 <211> 423
 <212> PRT
 <213> Homo sapiens

<400> 269

Met	Met	Tyr	Arg	Pro	Asp	Val	Val	Arg	Ala	Arg	Lys	Arg	Val	Cys	1	5	10	15
Trp	Glu	Pro	Trp	Val	Ile	Gly	Leu	Val	Ile	Phe	Ile	Ser	Leu	Ile	20	25	30	
Val	Leu	Ala	Val	Cys	Ile	Gly	Leu	Thr	Val	His	Tyr	Val	Arg	Tyr	35	40	45	
Asn	Gln	Lys	Lys	Thr	Tyr	Asn	Tyr	Tyr	Ser	Thr	Leu	Ser	Phe	Thr	50	55	60	
Thr	Asp	Lys	Leu	Tyr	Ala	Glu	Phe	Gly	Arg	Glu	Ala	Ser	Asn	Asn	65	70	75	
Phe	Thr	Glu	Met	Ser	Gln	Arg	Leu	Glu	Ser	Met	Val	Lys	Asn	Ala	80	85	90	
Phe	Tyr	Lys	Ser	Pro	Leu	Arg	Glu	Glu	Phe	Val	Lys	Ser	Gln	Val	95	100	105	
Ile	Lys	Phe	Ser	Gln	Gln	Lys	His	Gly	Val	Leu	Ala	His	Met	Leu	110	115	120	
Leu	Ile	Cys	Arg	Phe	His	Ser	Thr	Glu	Asp	Pro	Glu	Thr	Val	Asp	125	130	135	
Lys	Ile	Val	Gln	Leu	Val	Leu	His	Glu	Lys	Leu	Gln	Asp	Ala	Val	140	145	150	
Gly	Pro	Pro	Lys	Val	Asp	Pro	His	Ser	Val	Lys	Ile	Lys	Lys	Ile	155	160	165	
Asn	Lys	Thr	Glu	Thr	Asp	Ser	Tyr	Leu	Asn	His	Cys	Cys	Gly	Thr	170	175	180	
Arg	Arg	Ser	Lys	Thr	Leu	Gly	Gln	Ser	Leu	Arg	Ile	Val	Gly	Gly	185	190	195	
Thr	Glu	Val	Glu	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Leu	Gln	200	205	210	
Trp	Asp	Gly	Ser	His	Arg	Cys	Gly	Ala	Thr	Leu	Ile	Asn	Ala	Thr	215	220	225	

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cgaccactgc cgacacctgc aggtgccctg caaggagcta cagaggggtcg 350
ggccggcggc ctgcctgtgc ccaggactct ccagccccgc ccagccgccc 400
gacccgccgc gcatgggaga agtgcgcatg gcggccgaag agggccgcgc 450
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<210> 271

<211> 238

<212> PRT

<213> Homo sapiens

<400> 271

Met	Leu	Gly	Ser	Pro	Cys	Leu	Leu	Trp	Leu	Leu	Ala	Val	Thr	Phe
1				5				10						15
Leu	Val	Pro	Arg	Ala	Gln	Pro	Leu	Ala	Pro	Gln	Asp	Phe	Glu	Glu
				20				25						30
Glu	Glu	Ala	Asp	Glu	Thr	Glu	Thr	Ala	Trp	Pro	Pro	Leu	Pro	Ala
				35				40						45
Val	Pro	Cys	Asp	Tyr	Asp	His	Cys	Arg	His	Leu	Gln	Val	Pro	Cys
				50				55						60
Lys	Glu	Leu	Gln	Arg	Val	Gly	Pro	Ala	Ala	Cys	Leu	Cys	Pro	Gly
				65				70						75

caaaaaaaaaaaa aaa 2063

<210> 275

<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

Met Leu Gln Asp Pro Asp Ser Asp Gln Pro Leu Asn Ser Leu Asp
1 5 10 15

Val Lys Pro Leu Arg Lys Pro Arg Ile Pro Met Glu Thr Phe Arg
20 25 30

Lys Val Gly Ile Pro Ile Ile Ile Ala Leu Leu Ser Leu Ala Ser
35 40 45

Ile Ile Ile Val Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr
50 55 60

Tyr Phe Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln
65 70 75

Leu Cys Asp Gly Glu Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu
80 85 90

His Cys Val Lys Ser Phe Pro Glu Gly Pro Ala Val Ala Val Arg
95 100 105

Leu Ser Lys Asp Arg Ser Thr Leu Gln Val Leu Asp Ser Ala Thr
110 115 120

Gly Asn Trp Phe Ser Ala Cys Phe Asp Asn Phe Thr Glu Ala Leu
125 130 135

Ala Glu Thr Ala Cys Arg Gln Met Gly Tyr Ser Arg Ala Val Glu
140 145 150

Ile Gly Pro Asp Gln Asp Leu Asp Val Val Glu Ile Thr Glu Asn
155 160 165

Ser Gln Glu Leu Arg Met Arg Asn Ser Ser Gly Pro Cys Leu Ser
170 175 180

Gly Ser Leu Val Ser Leu His Cys Leu Ala Cys Gly Lys Ser Leu
185 190 195

Lys Thr Pro Arg Val Val Gly Gly Glu Glu Ala Ser Val Asp Ser
200 205 210

Trp Pro Trp Gln Val Ser Ile Gln Tyr Asp Lys Gln His Val Cys
215 220 225

Gly Gly Ser Ile Leu Asp Pro His Trp Val Leu Thr Ala Ala His
230 235 240

Cys Phe Arg Lys His Thr Asp Val Phe Asn Trp Lys Val Arg Ala
245 250 255

Gly Ser Asp Lys	Leu Gly Ser Phe Pro	Ser Leu Ala Val Ala Lys	260	265	270
Ile Ile Ile Ile	Glu Phe Asn Pro Met	Tyr Pro Lys Asp Asn Asp	275	280	285
Ile Ala Leu Met	Lys Leu Gln Phe Pro	Leu Thr Phe Ser Gly Thr	290	295	300
Val Arg Pro Ile	Cys Leu Pro Phe Phe	Asp Glu Glu Leu Thr Pro	305	310	315
Ala Thr Pro Leu	Trp Ile Ile Gly Trp	Gly Phe Thr Lys Gln Asn	320	325	330
Gly Gly Lys Met	Ser Asp Ile Leu Leu	Gln Ala Ser Val Gln Val	335	340	345
Ile Asp Ser Thr	Arg Cys Asn Ala Asp	Asp Ala Tyr Gln Gly Glu	350	355	360
Val Thr Glu Lys	Met Met Cys Ala Gly	Ile Pro Glu Gly Gly Val	365	370	375
Asp Thr Cys Gln	Gly Asp Ser Gly Gly	Pro Leu Met Tyr Gln Ser	380	385	390
Asp Gln Trp His	Val Val Gly Ile Val	Ser Trp Gly Tyr Gly Cys	395	400	405
Gly Gly Pro Ser	Thr Pro Gly Val Tyr	Thr Lys Val Ser Ala Tyr	410	415	420
Leu Asn Trp Ile	Tyr Asn Val Trp Lys	Ala Glu Leu	425	430	

<210> 276
 <211> 3143
 <212> DNA
 <213> Homo sapiens

<400> 276
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 gagcatggcc ctcccagccc tgggcctgga cccctggagc ctctgtggcc 150
 ttttcctctt ccaactgctt cagctgctgc tgccgacgac gaccgcgggg 200
 ggaggcgggc agggggcccat gccaggggtc agatactatg caggggatga 250
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 ctctgtctct gagtgggtgat ggaaatactc tctacgtggg ggctcgagaa 350
 gccattotgg ccttgatat ccaggatcca ggggtcccca ggctaaagaa 400

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agaagcctct tccactgtct acaatggctc cctcttgctg atagtgcagg 1950
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ccagggtcag tggggtggcc gccctggctg cccagcagtc ctactggccc 2150
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tcttgcttca gttggggcag actctgatcc cttctgccct ggcagaatgg 3000
caggggtaat ctgagccttc ttcactcctt taccctagct gacccttca 3050
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agagactgtt tattttttat taaaaatata aggcttaaaa aaa 3143

<210> 277

<211> 761

<212> PRT

<213> Homo sapiens

<400> 277

Met	Ala	Leu	Pro	Ala	Leu	Gly	Leu	Asp	Pro	Trp	Ser	Leu	Leu	Gly	1	5	10	15
Leu	Phe	Leu	Phe	Gln	Leu	Leu	Gln	Leu	Leu	Leu	Pro	Thr	Thr	Thr	20	25	30	
Ala	Gly	Gly	Gly	Gly	Gln	Gly	Pro	Met	Pro	Arg	Val	Arg	Tyr	Tyr	35	40	45	
Ala	Gly	Asp	Glu	Arg	Arg	Ala	Leu	Ser	Phe	Phe	His	Gln	Lys	Gly	50	55	60	
Leu	Gln	Asp	Phe	Asp	Thr	Leu	Leu	Leu	Ser	Gly	Asp	Gly	Asn	Thr	65	70	75	
Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Ile	Leu	Ala	Leu	Asp	Ile	Gln	80	85	90	
Asp	Pro	Gly	Val	Pro	Arg	Leu	Lys	Asn	Met	Ile	Pro	Trp	Pro	Ala	95	100	105	
Ser	Asp	Arg	Lys	Lys	Ser	Glu	Cys	Ala	Phe	Lys	Lys	Lys	Ser	Asn	110	115	120	
Glu	Thr	Gln	Cys	Phe	Asn	Phe	Ile	Arg	Val	Leu	Val	Ser	Tyr	Asn	125	130	135	
Val	Thr	His	Leu	Tyr	Thr	Cys	Gly	Thr	Phe	Ala	Phe	Ser	Pro	Ala	140	145	150	
Cys	Thr	Phe	Ile	Glu	Leu	Gln	Asp	Ser	Tyr	Leu	Leu	Pro	Ile	Ser	155	160	165	
Glu	Asp	Lys	Val	Met	Glu	Gly	Lys	Gly	Gln	Ser	Pro	Phe	Asp	Pro	170	175	180	
Ala	His	Lys	His	Thr	Ala	Val	Leu	Val	Asp	Gly	Met	Leu	Tyr	Ser	185	190	195	
Gly	Thr	Met	Asn	Asn	Phe	Leu	Gly	Ser	Glu	Pro	Ile	Leu	Met	Arg	200	205	210	
Thr	Leu	Gly	Ser	Gln	Pro	Val	Leu	Lys	Thr	Asp	Asn	Phe	Leu	Arg	215	220	225	
Trp	Leu	His	His	Asp	Ala	Ser	Phe	Val	Ala	Ala	Ile	Pro	Ser	Thr	230	235	240	
Gln	Val	Val	Tyr	Phe	Phe	Phe	Glu	Glu	Thr	Ala	Ser	Glu	Phe	Asp	245	250	255	
Phe	Phe	Glu	Arg	Leu	His	Thr	Ser	Arg	Val	Ala	Arg	Val	Cys	Lys	260	265	270	
Asn	Asp	Val	Gly	Gly	Glu	Lys	Leu	Leu	Gln	Lys	Lys	Trp	Thr	Thr	275	280	285	
Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Thr	Gln	Pro	Gly	Gln	Leu	Pro				

				290					295					300
Phe	Asn	Val	Ile	Arg 305	His	Ala	Val	Leu	Leu 310	Pro	Ala	Asp	Ser	Pro 315
Thr	Ala	Pro	His	Ile 320	Tyr	Ala	Val	Phe	Thr 325	Ser	Gln	Trp	Gln	Val 330
Gly	Gly	Thr	Arg	Ser 335	Ser	Ala	Val	Cys	Ala 340	Phe	Ser	Leu	Leu	Asp 345
Ile	Glu	Arg	Val	Phe 350	Lys	Gly	Lys	Tyr	Lys 355	Glu	Leu	Asn	Lys	Glu 360
Thr	Ser	Arg	Trp	Thr 365	Thr	Tyr	Arg	Gly	Pro 370	Glu	Thr	Asn	Pro	Arg 375
Pro	Gly	Ser	Cys	Ser 380	Val	Gly	Pro	Ser	Ser 385	Asp	Lys	Ala	Leu	Thr 390
Phe	Met	Lys	Asp	His 395	Phe	Leu	Met	Asp	Glu 400	Gln	Val	Val	Gly	Thr 405
Pro	Leu	Leu	Val	Lys 410	Ser	Gly	Val	Glu	Tyr 415	Thr	Arg	Leu	Ala	Val 420
Glu	Thr	Ala	Gln	Gly 425	Leu	Asp	Gly	His	Ser 430	His	Leu	Val	Met	Tyr 435
Leu	Gly	Thr	Thr	Thr 440	Gly	Ser	Leu	His	Lys 445	Ala	Val	Val	Ser	Gly 450
Asp	Ser	Ser	Ala	His 455	Leu	Val	Glu	Glu	Ile 460	Gln	Leu	Phe	Pro	Asp 465
Pro	Glu	Pro	Val	Arg 470	Asn	Leu	Gln	Leu	Ala 475	Pro	Thr	Gln	Gly	Ala 480
Val	Phe	Val	Gly	Phe 485	Ser	Gly	Gly	Val	Trp 490	Arg	Val	Pro	Arg	Ala 495
Asn	Cys	Ser	Val	Tyr 500	Glu	Ser	Cys	Val	Asp 505	Cys	Val	Leu	Ala	Arg 510
Asp	Pro	His	Cys	Ala 515	Trp	Asp	Pro	Glu	Ser 520	Arg	Thr	Cys	Cys	Leu 525
Leu	Ser	Ala	Pro	Asn 530	Leu	Asn	Ser	Trp	Lys 535	Gln	Asp	Met	Glu	Arg 540
Gly	Asn	Pro	Glu	Trp 545	Ala	Cys	Ala	Ser	Gly 550	Pro	Met	Ser	Arg	Ser 555
Leu	Arg	Pro	Gln	Ser 560	Arg	Pro	Gln	Ile	Ile 565	Lys	Glu	Val	Leu	Ala 570
Val	Pro	Asn	Ser	Ile 575	Leu	Glu	Leu	Pro	Cys 580	Pro	His	Leu	Ser	Ala 585

270

<400> 279
gtctgttcct ggctgtccac ccag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 280
catcttgtca tgtacctggg aaccaccaca gggtogetcc acaag 45

<210> 281
<211> 2320
<212> DNA
<213> Homo sapiens

<400> 281
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cttccgtaga agtgagcatg gctgggcagc gagtgcttct totagtgggc 100
ttccttctcc ctggggctct gctctcagag gctgccaaaa tcttgacaat 150
atctacagta ggtggaagcc attatctact gatggaccgg gtttctcaga 200
ttcttcaaga tcacgggtcat aatgtcacca tgcttaacca caaaagaggt 250
ccttttatgc cagattttta aaaggaagaa aaatcatatc aagttatcag 300
ttggcttgca cctgaagatc atcaaagaga atttaaaaag agttttgatt 350
tctttctgga agaaacttta ggtggcagag gaaaatttga aaacttatta 400
aatgttctag aatacttggc gttgcagtgc agtcattttt taaatagaaa 450
ggatatcatg gattccttaa agaattgagaa ctctgacatg gtgatagttg 500
aaacttttga ctactgtcct ttcttgattg ctgagaagct tgggaagcca 550
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aggaggcaac agcacatgca gtctacattt gacaacacca tcaaggaaca 750
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<210> 282
 <211> 523
 <212> PRT
 <213> Homo sapiens

<400> 282

Met	Ala	Gly	Gln	Arg	Val	Leu	Leu	Leu	Val	Gly	Phe	Leu	Leu	Pro
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Gly	Val	Leu	Leu	Ser	Glu	Ala	Ala	Lys	Ile	Leu	Thr	Ile	Ser	Thr
				20					25					30
Val	Gly	Gly	Ser	His	Tyr	Leu	Leu	Met	Asp	Arg	Val	Ser	Gln	Ile
				35					40					45
Leu	Gln	Asp	His	Gly	His	Asn	Val	Thr	Met	Leu	Asn	His	Lys	Arg
				50					55					60
Gly	Pro	Phe	Met	Pro	Asp	Phe	Lys	Lys	Glu	Glu	Lys	Ser	Tyr	Gln
				65					70					75
Val	Ile	Ser	Trp	Leu	Ala	Pro	Glu	Asp	His	Gln	Arg	Glu	Phe	Lys
				80					85					90
Lys	Ser	Phe	Asp	Phe	Phe	Leu	Glu	Glu	Thr	Leu	Gly	Gly	Arg	Gly
				95					100					105
Lys	Phe	Glu	Asn	Leu	Leu	Asn	Val	Leu	Glu	Tyr	Leu	Ala	Leu	Gln
				110					115					120
Cys	Ser	His	Phe	Leu	Asn	Arg	Lys	Asp	Ile	Met	Asp	Ser	Leu	Lys
				125					130					135
Asn	Glu	Asn	Phe	Asp	Met	Val	Ile	Val	Glu	Thr	Phe	Asp	Tyr	Cys
				140					145					150
Pro	Phe	Leu	Ile	Ala	Glu	Lys	Leu	Gly	Lys	Pro	Phe	Val	Ala	Ile
				155					160					165
Leu	Ser	Thr	Ser	Phe	Gly	Ser	Leu	Glu	Phe	Gly	Leu	Pro	Ile	Pro
				170					175					180
Leu	Ser	Tyr	Val	Pro	Val	Phe	Arg	Ser	Leu	Leu	Thr	Asp	His	Met
				185					190					195
Asp	Phe	Trp	Gly	Arg	Val	Lys	Asn	Phe	Leu	Met	Phe	Phe	Ser	Phe
				200					205					210
Cys	Arg	Arg	Gln	Gln	His	Met	Gln	Ser	Thr	Phe	Asp	Asn	Thr	Ile
				215					220					225
Lys	Glu	His	Phe	Thr	Glu	Gly	Ser	Arg	Pro	Val	Leu	Ser	His	Leu
				230					235					240
Leu	Leu	Lys	Ala	Glu	Leu	Trp	Phe	Ile	Asn	Ser	Asp	Phe	Ala	Phe
				245					250					255
Asp	Phe	Ala	Arg	Pro	Leu	Leu	Pro	Asn	Thr	Val	Tyr	Val	Gly	Gly

				260					265					270
Leu	Met	Glu	Lys	Pro 275	Ile	Lys	Pro	Val	Pro 280	Gln	Asp	Leu	Glu	Asn 285
Phe	Ile	Ala	Lys	Phe 290	Gly	Asp	Ser	Gly	Phe 295	Val	Leu	Val	Thr	Leu 300
Gly	Ser	Met	Val	Asn 305	Thr	Cys	Gln	Asn	Pro 310	Glu	Ile	Phe	Lys	Glu 315
Met	Asn	Asn	Ala	Phe 320	Ala	His	Leu	Pro	Gln 325	Gly	Val	Ile	Trp	Lys 330
Cys	Gln	Cys	Ser	His 335	Trp	Pro	Lys	Asp	Val 340	His	Leu	Ala	Ala	Asn 345
Val	Lys	Ile	Val	Asp 350	Trp	Leu	Pro	Gln	Ser 355	Asp	Leu	Leu	Ala	His 360
Pro	Ser	Ile	Arg	Leu 365	Phe	Val	Thr	His	Gly 370	Gly	Gln	Asn	Ser	Ile 375
Met	Glu	Ala	Ile	Gln 380	His	Gly	Val	Pro	Met 385	Val	Gly	Ile	Pro	Leu 390
Phe	Gly	Asp	Gln	Pro 395	Glu	Asn	Met	Val	Arg 400	Val	Glu	Ala	Lys	Lys 405
Phe	Gly	Val	Ser	Ile 410	Gln	Leu	Lys	Lys	Leu 415	Lys	Ala	Glu	Thr	Leu 420
Ala	Leu	Lys	Met	Lys 425	Gln	Ile	Met	Glu	Asp 430	Lys	Arg	Tyr	Lys	Ser 435
Ala	Ala	Val	Ala	Ala 440	Ser	Val	Ile	Leu	Arg 445	Ser	His	Pro	Leu	Ser 450
Pro	Thr	Gln	Arg	Leu 455	Val	Gly	Trp	Ile	Asp 460	His	Val	Leu	Gln	Thr 465
Gly	Gly	Ala	Thr	His 470	Leu	Lys	Pro	Tyr	Val 475	Phe	Gln	Gln	Pro	Trp 480
His	Glu	Gln	Tyr	Leu 485	Phe	Asp	Val	Phe	Val 490	Phe	Leu	Leu	Gly	Leu 495
Thr	Leu	Gly	Thr	Leu 500	Trp	Leu	Cys	Gly	Lys 505	Leu	Leu	Gly	Met	Ala 510
Val	Trp	Trp	Leu	Arg 515	Gly	Ala	Arg	Lys	Val 520	Lys	Glu	Thr		

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<210> 283
<211> 24
<212> DNA
<213> Artificial
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<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.
 <400> 283
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<210> 284
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 284
 tcaggctggt ctccaaagag aggg 24

<210> 285
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 285
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<210> 286
 <211> 2340
 <212> DNA
 <213> Homo sapiens

<400> 286
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 gtgctgtccc atccagcagg gctaccctga agctctggct gcagccctcc 200
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 gagtaagagt gggaggcagg acagagctgg gacacaggta tggagagggg 350
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ccacctcctg aaactgctcc acctttgaag tttgaacttt agtccctcca 1950
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 cattccttca gaccctctcc tgccagtatg ctaaaccctc cctctctctt 2150
 tcttatcccg ctgtcccatt ggcccagcct ggatgaatct atcaataaaa 2200
 caactagaga atgggtgtca gtgagacact atagaattac taaggagaag 2250
 atgcctctgg agtttggatc ggggtgttaca ggtacaagta ggtatgttgc 2300
 agaggaaaat aaatatcaaa ctgtatacta aaattaaaaa 2340

<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

Met	Leu	Gly	Ala	Lys	Pro	His	Trp	Leu	Pro	Gly	Pro	Leu	His	Ser
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Pro	Gly	Leu	Pro	Leu	Val	Leu	Val	Leu	Leu	Ala	Leu	Gly	Ala	Gly
				20					25					30
Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys
				35					40					45
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly
				50					55					60
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala
				65					70					75
Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn
				80					85					90
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu
				95					100					105
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val
				110					115					120
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn
				125					130					135
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val
				140					145					150
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala
				155					160					165
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser

	170		175		180
Leu Arg Leu Arg Arg Gly Asn Leu Leu Gly Gly Trp Lys Tyr Ser					
	185		190		195
Ser Phe Ser Gly Phe Leu Ile Phe Pro Leu					
	200		205		

<210> 288
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 288
 aggagccac cagctctgtg ctac 24

<210> 289
 <211> 27
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-27
 <223> Synthetic construct.

<400> 289
 cagagaggga agatgaggaa gccagag 27

<210> 290
 <211> 42
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-42
 <223> Synthetic construct.

<400> 290
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<210> 291
 <211> 1570
 <212> DNA
 <213> Homo sapiens

<400> 291
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ttcccgcggg gccgtgactg ggcgggcttc agccatgaag accctcatag 200
 ccgcctactc cggggctcctg cgcgggcgagc gtcaggccga ggctgaccgg 250
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 aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa 1550
 aaaaaaaaa aaaaaaaaa 1570

<210> 292
 <211> 388
 <212> PRT
 <213> Homo sapiens

<400> 292

Met	Lys	Thr	Leu	Ile	Ala	Ala	Tyr	Ser	Gly	Val	Leu	Arg	Gly	Glu
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Arg	Gln	Ala	Glu	Ala	Asp	Arg	Ser	Gln	Arg	Ser	His	Gly	Gly	Pro
				20					25					30
Ala	Leu	Ser	Arg	Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser
				35					40					45
Ile	Leu	Ser	Ala	Leu	Gln	Asp	Leu	Phe	Ser	Val	Thr	Trp	Leu	Asn
				50					55					60
Arg	Ser	Lys	Val	Glu	Lys	Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln
				65					70					75
Trp	Val	Leu	Ser	Phe	Leu	Val	Leu	Gly	Val	Ala	Cys	Ser	Ala	Ile
				80					85					90
Leu	Met	Tyr	Ile	Phe	Cys	Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu
				95					100					105
Tyr	Phe	Thr	Trp	Leu	Val	Phe	Asp	Trp	Asn	Thr	Pro	Lys	Lys	Gly
				110					115					120
Gly	Arg	Arg	Ser	Gln	Trp	Val	Arg	Asn	Trp	Ala	Val	Trp	Arg	Tyr
				125					130					135
Phe	Arg	Asp	Tyr	Phe	Pro	Ile	Gln	Leu	Val	Lys	Thr	His	Asn	Leu
				140					145					150
Leu	Thr	Thr	Arg	Asn	Tyr	Ile	Phe	Gly	Tyr	His	Pro	His	Gly	Ile
				155					160					165
Met	Gly	Leu	Gly	Ala	Phe	Cys	Asn	Phe	Ser	Thr	Glu	Ala	Thr	Glu
				170					175					180
Val	Ser	Lys	Lys	Phe	Pro	Gly	Ile	Arg	Pro	Tyr	Leu	Ala	Thr	Leu
				185					190					195
Ala	Gly	Asn	Phe	Arg	Met	Pro	Val	Leu	Arg	Glu	Tyr	Leu	Met	Ser
				200					205					210
Gly	Gly	Ile	Cys	Pro	Val	Ser	Arg	Asp	Thr	Ile	Asp	Tyr	Leu	Leu
				215					220					225
Ser	Lys	Asn	Gly	Ser	Gly	Asn	Ala	Ile	Ile	Ile	Val	Val	Gly	Gly
				230					235					240
Ala	Ala	Glu	Ser	Leu	Ser	Ser	Met	Pro	Gly	Lys	Asn	Ala	Val	Thr
				245					250					255
Leu	Arg	Asn	Arg	Lys	Gly	Phe	Val	Lys	Leu	Ala	Leu	Arg	His	Gly

<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 295
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<210> 296
<211> 3060
<212> DNA
<213> Homo sapiens

<400> 296
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cgggggcgcg gaggcgacgc cggggacgcc cgcgcgacga gcaggtggcg 150
gcggctgcag gcttgtccag ccggaagccc tgagggcagc tgttcccact 200
ggctctgctg accttgtgcc ttggacggct gtcctcagcg agggggccgtg 250
caccgcctcc tgagcagcgc catgggcctg ctggccttcc tgaagaccca 300
gttcgtgctg cacctgctgg tcggctttgt cttcgtggtg agtggctctg 350
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cagctctacc gccgcctcaa ctgcgcctc gcctactcac tctggagcca 450
actggctcatg ctgctggagt ggtggtcctg cacggagtgt acactgttca 500
cggaccaggc cacggtagag cgctttggga aggagcacgc agtcatcatc 550
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<210> 297

<211> 368

<212> PRT

<213> Homo sapiens

<400> 297

Met	Gly	Leu	Leu	Ala	Phe	Leu	Lys	Thr	Gln	Phe	Val	Leu	His	Leu	1	5	10	15
Leu	Val	Gly	Phe	Val	Phe	Val	Val	Ser	Gly	Leu	Val	Ile	Asn	Phe	20	25	30	
Val	Gln	Leu	Cys	Thr	Leu	Ala	Leu	Trp	Pro	Val	Ser	Lys	Gln	Leu	35	40	45	
Tyr	Arg	Arg	Leu	Asn	Cys	Arg	Leu	Ala	Tyr	Ser	Leu	Trp	Ser	Gln	50	55	60	
Leu	Val	Met	Leu	Leu	Glu	Trp	Trp	Ser	Cys	Thr	Glu	Cys	Thr	Leu	65	70	75	
Phe	Thr	Asp	Gln	Ala	Thr	Val	Glu	Arg	Phe	Gly	Lys	Glu	His	Ala	80	85	90	
Val	Ile	Ile	Leu	Asn	His	Asn	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly	95	100	105	
Trp	Thr	Met	Cys	Glu	Arg	Phe	Gly	Val	Leu	Gly	Ser	Ser	Lys	Val	110	115	120	
Leu	Ala	Lys	Lys	Glu	Leu	Leu	Tyr	Val	Pro	Leu	Ile	Gly	Trp	Thr	125	130	135	
Trp	Tyr	Phe	Leu	Glu	Ile	Val	Phe	Cys	Lys	Arg	Lys	Trp	Glu	Glu	140	145	150	
Asp	Arg	Asp	Thr	Val	Val	Glu	Gly	Leu	Arg	Arg	Leu	Ser	Asp	Tyr	155	160	165	

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-21

<223> Synthetic construct.

<400> 299

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<210> 300

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 300

ccaaggtcct cgctaagaag gagctgctct acgtgccct catcg 45

<210> 301

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 301

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tcagtttgtc ttgtgggggtt ggtggcaggc aggccggctt acgcctgata 200

cggccctggg ttagaaggga agggaagata aacttttata caaatgggga 250

tagctgggggt ctgagacctg cttoctcagt aaaattcctg ggatctgcct 300

ataccttctt ttctctaacc tggcataccc tgcttaaagc ctctcagggc 350

ttctctctgt tcttaggata aaagtattta gagctacaag agccctcatg 400

gtctggcccc tgccccctg gccagcttca ttgtacatgt ggtgttctct 450

tgtocttctt gtaatgtgggt atgccatggg gtctttgcac aagcctttcc 500

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atgtagtcat cctgcagatt tcaattctaa catcattttc tccagggata 600

ctggcctgac agaattctcat cttgtttaat gctctcataa gaccatttgt 650

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gttgatatggg ttgtgtctgt tcccagaat gccagctct gagctgcgtg 750

<210> 303
 <211> 1768
 <212> DNA
 <213> Homo sapiens

<400> 303
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<210> 308

<211> 671

<212> PRT

<213> Homo sapiens

<400> 308

Met	Pro	His	Ala	Phe	Lys	Pro	Gly	Asp	Leu	Val	Phe	Ala	Lys	Met
1				5					10					15
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Gly	Cys	Asp	Arg	Ile 665	Ile	Gly	Ser	Lys	Lys 670	Lys	Phe	Asp	Lys	Cys 675
Met	Val	Cys	Gly	Gly 680	Asp	Gly	Ser	Gly	Cys 685	Ser	Lys	Gln	Ser	Gly 690
Ser	Phe	Arg	Lys	Phe 695	Arg	Tyr	Gly	Tyr	Asn 700	Asn	Val	Val	Thr	Ile 705
Pro	Ala	Gly	Ala	Thr 710	His	Ile	Leu	Val	Arg 715	Gln	Gln	Gly	Asn	Pro 720
Gly	His	Arg	Ser	Ile	Tyr	Leu	Ala	Leu	Lys	Leu	Pro	Asp	Gly	Ser

	725		730		735
Tyr Ala Leu Asn Gly Glu Tyr Thr Leu Met Pro Ser Pro Thr Asp					
	740		745		750
Val Val Leu Pro Gly Ala Val Ser Leu Arg Tyr Ser Gly Ala Thr					
	755		760		765
Ala Ala Ser Glu Thr Leu Ser Gly His Gly Pro Leu Ala Gln Pro					
	770		775		780
Leu Thr Leu Gln Val Leu Val Ala Gly Asn Pro Gln Asp Thr Arg					
	785		790		795
Leu Arg Tyr Ser Phe Phe Val Pro Arg Pro Thr Pro Ser Thr Pro					
	800		805		810
Arg Pro Thr Pro Gln Asp Trp Leu His Arg Arg Ala Gln Ile Leu					
	815		820		825
Glu Ile Leu Arg Arg Arg Pro Trp Ala Gly Arg Lys					
	830		835		

<210> 318
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 318
 ccctgaagct gccagatggc tcc 23

<210> 319
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 319
 ctgtgctctt cggcgcagcc agtc 24

<210> 320
 <211> 43
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-43
 <223> Synthetic construct.

<400> 320
ccacagatgt ggtactgcct ggggcagtca gcttgcgcta cag 43

<210> 321
<211> 1197
<212> DNA
<213> Homo sapiens

<400> 321
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gagagaccat ggcaaagaat cctccagaga attgtgaaga ctgtcacatt 100
ctaaatgcag aagcttttaa atccaagaaa atatgtaaat cacttaagat 150
ttgtggactg gtgttttgta tcttggccct aactctaatt gtctgtttt 200
gggggagcaa gcacttctgg ccggaggtag ccaaaaaagc ctatgacatg 250
gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300
tgatcctgtg accagaactg aaatattcag aagcggaaat ggcactgatg 350
aaacattgga agtgcacgac tttaaaaacg gatacactgg catctacttc 400
gtgggtcttc aaaaatgttt tatcaaaact cagattaaag tgattcctga 450
atcttctgaa ccagaagagg aaatagatga gaatgaagaa attaccacaa 500
ctttctttga acagtcagtg atttgggtcc cagcagaaaa gcctattgaa 550
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gaccgcgtcac gccagacaag caagtgagga agaacttcca ataatgact 800
atactgaaaa tggaatagaa tttgatccca tgcgtgatga gagaggttat 850
tgttgtattt actgccgtcg aggcaaccgc tattgccgcc gcgtctgtga 900
acctttacta ggctactacc catatccata ctgctaccaa ggaggacgag 950
tcatctgtcg tgtcatcatg ccttctaact ggtgggtggc ccgcatgctg 1000
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atataataaa tgcattgctat tcaatgaatt tctgcctatg aggcattctg 1100
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tgttctaata aacttctaca ttatcaccaa aaaaaaaaaa aaaaaaa 1197

<210> 322

<211> 317
 <212> PRT
 <213> Homo sapiens

<400> 322

Met	Ala	Lys	Asn	Pro	Pro	Glu	Asn	Cys	Glu	Asp	Cys	His	Ile	Leu	1	5	10	15
Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys	20	25	30	
Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val	35	40	45	
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys	50	55	60	
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys	65	70	75	
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe	80	85	90	
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe	95	100	105	
Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys	110	115	120	
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro	125	130	135	
Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe	140	145	150	
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn	155	160	165	
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn	170	175	180	
Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu	185	190	195	
Leu	Gln	Asp	Phe	Glu	Glu	Glu	Gly	Glu	Asp	Leu	His	Phe	Pro	Ala	200	205	210	
Asn	Glu	Lys	Lys	Gly	Ile	Glu	Gln	Asn	Glu	Gln	Trp	Val	Val	Pro	215	220	225	
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu	230	235	240	
Glu	Glu	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe	245	250	255	
Asp	Pro	Met	Leu	Asp	Glu	Arg	Gly	Tyr	Cys	Cys	Ile	Tyr	Cys	Arg	260	265	270	

ataccaaaga ctgaaaaaaa aaatcctgtc tgtttttgta tttattatat 1050
 atatttatgt gggtgatttg ataacaagtt taatataaag tgacttggga 1100
 gtttggtcag tggggttggt ttgtgatcca ggaataaacc ttgcggatgt 1150
 ggctgtttat gaaaaaaaaa aaaa 1174

<210> 324

<211> 239

<212> PRT

<213> Homo sapiens

<400> 324

Met	Ala	Ser	Thr	Ala	Val	Gln	Leu	Leu	Gly	Phe	Leu	Leu	Ser	Phe	1	5	10	15
Leu	Gly	Met	Val	Gly	Thr	Leu	Ile	Thr	Thr	Ile	Leu	Pro	His	Trp	20	25	30	
Arg	Arg	Thr	Ala	His	Val	Gly	Thr	Asn	Ile	Leu	Thr	Ala	Val	Ser	35	40	45	
Tyr	Leu	Lys	Gly	Leu	Trp	Met	Glu	Cys	Val	Trp	His	Ser	Thr	Gly	50	55	60	
Ile	Tyr	Gln	Cys	Gln	Ile	Tyr	Arg	Ser	Leu	Leu	Ala	Leu	Pro	Gln	65	70	75	
Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Met	Val	Ile	Ser	Cys	Leu	Leu	80	85	90	
Ser	Gly	Ile	Ala	Cys	Ala	Cys	Ala	Val	Ile	Gly	Met	Lys	Cys	Thr	95	100	105	
Arg	Cys	Ala	Lys	Gly	Thr	Pro	Ala	Lys	Thr	Thr	Phe	Ala	Ile	Leu	110	115	120	
Gly	Gly	Thr	Leu	Phe	Ile	Leu	Ala	Gly	Leu	Leu	Cys	Met	Val	Ala	125	130	135	
Val	Ser	Trp	Thr	Thr	Asn	Asp	Val	Val	Gln	Asn	Phe	Tyr	Asn	Pro	140	145	150	
Leu	Leu	Pro	Ser	Gly	Met	Lys	Phe	Glu	Ile	Gly	Gln	Ala	Leu	Tyr	155	160	165	
Leu	Gly	Phe	Ile	Ser	Ser	Ser	Leu	Ser	Leu	Ile	Gly	Gly	Thr	Leu	170	175	180	
Leu	Cys	Leu	Ser	Cys	Gln	Asp	Glu	Ala	Pro	Tyr	Arg	Pro	Tyr	Gln	185	190	195	
Ala	Pro	Pro	Arg	Ala	Thr	Thr	Thr	Thr	Ala	Asn	Thr	Ala	Pro	Ala	200	205	210	
Tyr	Gln	Pro	Pro	Ala	Ala	Tyr	Lys	Asp	Asn	Arg	Ala	Pro	Ser	Val	215	220	225	

Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val
 230 235

<210> 325
 <211> 2121
 <212> DNA
 <213> Homo sapiens

<400> 325
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 ggcagcttct cgcaggcggc agggcgggcg gccaggatca tgtccaccac 100
 cacatgccaa gtggtggcgt tcctcctgtc catcctgggg ctggccggct 150
 gcatcgcggc caccgggatg gacatgtgga gcacccagga cctgtacgac 200
 aaccccgctca cctccgtgtt ccagtacgaa gggctctgga ggagctgcgt 250
 gaggcagagt tcaggcttca ccgaatgcag gccctatttc accatcctgg 300
 gacttcacgc catgctgcag gcagtgcgag ccctgatgat cgtaggcatc 350
 gtccctgggtg ccattggcct cctggatatcc atctttgccc tgaaatgcat 400
 ccgcattggc agcatggagg actctgccaa agccaacatg aactgacct 450
 ccgggatcat gttcattgtc tcaggctctt gtgcaattgc tggagtgtct 500
 gtgtttgcc aatgctggt gactaacttc tggatgtcca cagctaacat 550
 gtacaccggc atgggtggga tgggtgcagac tgttcagacc aggtacacat 600
 ttggtgcggc tctgttcgtg ggctgggtcg ctggaggcct cacactaatt 650
 gggggtgtga tgatgtgcat cgcctgccgg ggctggcac cagaagaaac 700
 caactacaaa gccgtttctt atcatgcctc aggccacagt gttgcctaca 750
 agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaac 800
 aagaagatat acgatggagg tgcccgaca gaggacgagg tacaatctta 850
 tccttccaag cagcactatg tgtaatgtc taagacctct cagcacgggc 900
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 catctttgga gaggccaaat ggtcttagcc tcagtctctg tctctaaata 1050
 ttccaccata aaacagctga gttatttatg aattagaggc tatagctcac 1100
 attttcaatc ctctatttct ttttttaaata ataactttct actctgatga 1150
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 cccctcttct ctcctagtca ataaacccat tgatgatcta tttcccagct 1250

				80					85					90
Ala	Ile	Gly	Leu	Leu 95	Val	Ser	Ile	Phe	Ala 100	Leu	Lys	Cys	Ile	Arg 105
Ile	Gly	Ser	Met	Glu 110	Asp	Ser	Ala	Lys	Ala 115	Asn	Met	Thr	Leu	Thr 120
Ser	Gly	Ile	Met	Phe 125	Ile	Val	Ser	Gly	Leu 130	Cys	Ala	Ile	Ala	Gly 135
Val	Ser	Val	Phe	Ala 140	Asn	Met	Leu	Val	Thr 145	Asn	Phe	Trp	Met	Ser 150
Thr	Ala	Asn	Met	Tyr 155	Thr	Gly	Met	Gly	Gly 160	Met	Val	Gln	Thr	Val 165
Gln	Thr	Arg	Tyr	Thr 170	Phe	Gly	Ala	Ala	Leu 175	Phe	Val	Gly	Trp	Val 180
Ala	Gly	Gly	Leu	Thr 185	Leu	Ile	Gly	Gly	Val 190	Met	Met	Cys	Ile	Ala 195
Cys	Arg	Gly	Leu	Ala 200	Pro	Glu	Glu	Thr	Asn 205	Tyr	Lys	Ala	Val	Ser 210
Tyr	His	Ala	Ser	Gly 215	His	Ser	Val	Ala	Tyr 220	Lys	Pro	Gly	Gly	Phe 225
Lys	Ala	Ser	Thr	Gly 230	Phe	Gly	Ser	Asn	Thr 235	Lys	Asn	Lys	Lys	Ile 240
Tyr	Asp	Gly	Gly	Ala 245	Arg	Thr	Glu	Asp	Glu 250	Val	Gln	Ser	Tyr	Pro 255
Ser	Lys	His	Asp	Tyr 260	Val									

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<210> 327
<211> 2010
<212> DNA
<213> Homo sapiens
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<400> 327
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gtagcagttc cggagtcacag ctggctaata ctcattccag aggataatgg 100
caacccatgc cttagaaatc gctgggctgt ttcttggtgg tgttggaatg 150
gtgggcacag tggtgtcac tgtcatgcct cagtggagag tgtcggcctt 200
cattgaaaac aacatcgtgg tttttgaaaa cttctgggaa ggactgtgga 250
tgaattgcgt gaggcaggct aacatcagga tgcaatgcaa aatctatgat 300
tccttctgtg ctctttctcc ggacctacag gcagccagag gaactgatgtg 350
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atttttgttc tgtgaaaaat aaatttcctt cttgtaccat ttctgttttag 1850
 ttttactaaa atctgtaaat actgtatttt tctgtttatt ccaaatttga 1900
 tgaaactgac aatccaattt gaaagtttgt gtcgacgtct gtctagctta 1950
 aatgaatgtg ttctatttgc tttatacatt tatattaata aattgtacat 2000
 ttttctaatt 2010

<210> 328

<211> 225

<212> PRT

<213> Homo sapiens

<400> 328

Met	Ala	Thr	His	Ala	Leu	Glu	Ile	Ala	Gly	Leu	Phe	Leu	Gly	Gly	1	5	10	15
Val	Gly	Met	Val	Gly	Thr	Val	Ala	Val	Thr	Val	Met	Pro	Gln	Trp	20	25	30	
Arg	Val	Ser	Ala	Phe	Ile	Glu	Asn	Asn	Ile	Val	Val	Phe	Glu	Asn	35	40	45	
Phe	Trp	Glu	Gly	Leu	Trp	Met	Asn	Cys	Val	Arg	Gln	Ala	Asn	Ile	50	55	60	
Arg	Met	Gln	Cys	Lys	Ile	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Ser	Pro	65	70	75	
Asp	Leu	Gln	Ala	Ala	Arg	Gly	Leu	Met	Cys	Ala	Ala	Ser	Val	Met	80	85	90	
Ser	Phe	Leu	Ala	Phe	Met	Met	Ala	Ile	Leu	Gly	Met	Lys	Cys	Thr	95	100	105	
Arg	Cys	Thr	Gly	Asp	Asn	Glu	Lys	Val	Lys	Ala	His	Ile	Leu	Leu	110	115	120	
Thr	Ala	Gly	Ile	Ile	Phe	Ile	Ile	Thr	Gly	Met	Val	Val	Leu	Ile	125	130	135	
Pro	Val	Ser	Trp	Val	Ala	Asn	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	140	145	150	
Ser	Ile	Val	Asn	Val	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Glu	Ala	Leu	155	160	165	
Tyr	Leu	Gly	Trp	Thr	Thr	Ala	Leu	Val	Leu	Ile	Val	Gly	Gly	Ala	170	175	180	
Leu	Phe	Cys	Cys	Val	Phe	Cys	Cys	Asn	Glu	Lys	Ser	Ser	Ser	Tyr	185	190	195	
Arg	Tyr	Ser	Ile	Pro	Ser	His	Arg	Thr	Thr	Gln	Lys	Ser	Tyr	His	200	205	210	

Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr	Val
				215					220					225

<210> 329
 <211> 1315
 <212> DNA
 <213> Homo sapiens

<400> 329
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 gaccgctttc atcggcaaca gcatcgtggt ggcccagggt gtgtgggagg 150
 gcctgtggat gtctgctgtg gtgcagagca ccggccagat gcagtgaag 200
 gtgtacgact cactgctggc gctgccacag gacctgcagg ctgcacgtgc 250
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 ttgctggggc caagtgtacc acctgtgtgg aggagaagga ttccaaggcc 350
 cgcttggtgc tcacctctgg gattgtcttt gtcattctcag gggctcctgac 400
 gctaattccc gtgtgctgga cggcgcatgc catcatccgg gacttctata 450
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 accaagaatt acgtctgacg tggaggggaa tgggggctcc gctggcgcta 700
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 ttttgtttct gcctcctgct atttttcttt tgactgagga tatttaaaat 800
 tcatttgaaa actgagccaa ggtgttgact cagactctca cttaggctct 850
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 aaaaacaaat catctgttaa caaaggactg cccacctccg gaacttttga 1150
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 cagctatgta gacccccgcc cccacctcca aactgcacc cttctgcct 1250

gccccctcg tctcaccccc tttaactca cattttttatc aaataaagca 1300

tgttttgtta gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ser	Ala	Gly	Met	Gln	Ile	Leu	Gly	Val	Val	Leu	Thr	Leu
1				5					10					15

Leu	Gly	Trp	Val	Asn	Gly	Leu	Val	Ser	Cys	Ala	Leu	Pro	Met	Trp
				20					25					30

Lys	Val	Thr	Ala	Phe	Ile	Gly	Asn	Ser	Ile	Val	Val	Ala	Gln	Val
				35					40					45

Val	Trp	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly
				50					55					60

Gln	Met	Gln	Cys	Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln
				65					70					75

Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Cys	Val	Ile	Ala	Leu	Leu	Val
				80					85					90

Ala	Leu	Phe	Gly	Leu	Leu	Val	Tyr	Leu	Ala	Gly	Ala	Lys	Cys	Thr
				95					100					105

Thr	Cys	Val	Glu	Glu	Lys	Asp	Ser	Lys	Ala	Arg	Leu	Val	Leu	Thr
				110					115					120

Ser	Gly	Ile	Val	Phe	Val	Ile	Ser	Gly	Val	Leu	Thr	Leu	Ile	Pro
				125					130					135

Val	Cys	Trp	Thr	Ala	His	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro
				140					145					150

Leu	Val	Ala	Glu	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ser	Leu	Tyr
				155					160					165

Leu	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Leu	Gly	Gly	Gly	Leu
				170					175					180

Leu	Cys	Cys	Thr	Cys	Pro	Ser	Gly	Gly	Ser	Gln	Gly	Pro	Ser	His
				185					190					195

Tyr	Met	Ala	Arg	Tyr	Ser	Thr	Ser	Ala	Pro	Ala	Ile	Ser	Arg	Gly
				200					205					210

Pro	Ser	Glu	Tyr	Pro	Thr	Lys	Asn	Tyr	Val
				215					220

<210> 331

<211> 1160

<212> DNA

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Tyr Ser Ser Leu	Leu Ala Leu Pro Pro Ala Leu Glu Thr Ala Arg		
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Ala Leu Met Cys Val	Ala Val Ala Leu Ser Leu Ile Ala Leu Leu		
	35	40	45
Ile Gly Ile Cys Gly	Met Lys Gln Val Gln Cys Thr Gly Ser Asn		
	50	55	60
Glu Arg Ala Lys Ala	Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe		
	65	70	75
Ile Leu Thr Gly Ile	Phe Val Leu Ile Pro Val Ser Trp Thr Ala		
	80	85	90
Asn Ile Ile Ile Arg	Asp Phe Tyr Asn Pro Ala Ile His Ile Gly		
	95	100	105
Gln Lys Arg Glu Leu	Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser		
	110	115	120
Ala Ala Val Leu Phe	Ile Gly Gly Gly Leu Leu Cys Gly Phe Cys		
	125	130	135
Cys Cys Asn Arg Lys	Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly		
	140	145	150
Tyr Arg Val Pro His	Thr Asp Lys Arg Arg Asn Thr Thr Met Leu		
	155	160	165
Ser Lys Thr Ser Thr	Ser Tyr Val		
	170		

<210> 333
 <211> 535
 <212> DNA
 <213> Homo sapiens

<400> 333
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 ctcagaagct gctagtctgt ctccaaaaaa agtggactgc agcatttaca 150
 agaagtatcc agtgggtggcc atcccctgcc ccatcacata octaccagtt 200
 tgtggttctg actacatcac ctatgggaat gaatgtcact tgtgtaccga 250
 gagcttgaaa agtaatggaa gagttcagtt tottcacgat ggaagttgct 300
 aaatttccca tggacataga gagaaaggaa tgatattctc atcatcatct 350
 tcatcatccc aggctctgac tgagtttctt tcagttttac tgatgttctg 400
 ggtggggggac agagccagat tcagagtaat cttgactgaa tggagaaagt 450

agccatggca	gctaccgaca	gcatgagagg	ggaggcccca	ggggcagaga	300
ccccagcct	gagacacaga	ggtcaagctg	cacagccaga	gcccgacacg	350
gggttcacag	caacaccgcc	agccccggac	tccccgcagg	agcccctcgt	400
gctacggctg	aaattcctca	atgattcaga	gcagggtggc	agggcctggc	450
cccacgacac	cattggctcc	ttgaaaagga	cccagtttcc	cggccgggaa	500
cagcaggtgc	gactcatcta	ccaagggcag	ctgctaggcg	acgacaccca	550
gaccctgggc	agccttcacc	tccctcccaa	ctgcgttctc	cactgccacg	600
tgtccacgag	agtcggtccc	ccaaatcccc	cctgcccggc	gggggtccgag	650
cccgccccct	ccgggctgga	aatcggcagc	ctgctgctgc	ccctgctgct	700
cctgctgttg	ctgctgctct	ggtactgcca	gatccagtac	cggcccttct	750
ttcccctgac	cgccactctg	ggcctggccg	gcttcaccct	gtcctcagt	800
ctcctggcct	ttgcatgta	ccgcccgtag	tgccctccgcg	ggcgcttggc	850
agcgtcgccg	gccccctccg	accttgctcc	ccgcgcgcgcg	gcgggagctg	900
ctgcctgccc	aggcccgcc	ctccggcctg	cctcttcccg	ctgccctgga	950
gcccgacct	gcgcgcgaga	ggactcccgg	gactggcgga	ggccccgccc	1000
tgcgaccgcc	ggggctcggg	gccacctccc	ggggctgctg	aacctcagcc	1050
cgcactggga	gtgggctcct	cggggtcggg	catctgctgt	cgctgcctcg	1100
gccccgggca	gagccggggc	gccccggggg	cccgctcttag	tgttctgccg	1150
gaggaccag	ccgcctccaa	tccctgacag	ctccttgggc	tgagttgggg	1200
acgccaggtc	ggtgggaggc	tggtgaaggg	gagcggggag	gggcagagga	1250
gttccccgga	acccgtgcag	attaaagtaa	ctgtgaagtt	ttaaaaaaaaa	1300
aaaaaaaaaa	1310				

<210> 338

<211> 246

<212> PRT

<213> Homo sapiens

<400> 338

Met Thr Leu Ile Glu Gly Val Gly Asp Glu Val Thr Val Leu Phe
1 5 10 15

Ser Val Leu Ala Cys Leu Leu Val Leu Ala Leu Ala Trp Val Ser
20 25 30

Thr His Thr Ala Glu Gly Gly Asp Pro Leu Pro Gln Pro Ser Gly
35 40 45

aggacttgga tgggtttgag gggtactccc tgagtgactg gctgtgcctg 300
gcttttgtgg aaagcaagtt caacatatca aagataaatg aaaatgcgga 350
tggaagcttt gactatggcc tcttcagat caacagccac tactggtgca 400
acgattataa gagttactcg gaaaaccttt gccacgtaga ctgtcaagat 450
ctgctgaatc ccaaccttct tgcaggcatc cactgcgcaa aaaggattgt 500
gtccggagca cgggggatga acaactgggt agaatggagg ttgactgtt 550
caggccggcc actctcctac tggctgacag gatgccgcct gagatgaaac 600
agggtgcggg tgcacgtgg agtcattcca agactcctgt cctcactcag 650
ggattcttca tttcttcttc ctactgcctc cacttcatgt tattttcttc 700
ccttcccatt tacaactaaa actgaccaga gcccagga taaatggttt 750
tcttggttc ctccttactc ccatctggac ccagtcccct gggtcctgtc 800
tggtattgt aaactgagga ccacaataaa gaaatcttta tatttatcg 849

<210> 340

<211> 148

<212> PRT

<213> Homo sapiens

<400> 340

Met	Thr	Lys	Ala	Leu	Leu	Ile	Tyr	Leu	Val	Ser	Ser	Phe	Leu	Ala
1				5					10					15
Leu	Asn	Gln	Ala	Ser	Leu	Ile	Ser	Arg	Cys	Asp	Leu	Ala	Gln	Val
				20					25					30
Leu	Gln	Leu	Glu	Asp	Leu	Asp	Gly	Phe	Glu	Gly	Tyr	Ser	Leu	Ser
				35					40					45
Asp	Trp	Leu	Cys	Leu	Ala	Phe	Val	Glu	Ser	Lys	Phe	Asn	Ile	Ser
				50					55					60
Lys	Ile	Asn	Glu	Asn	Ala	Asp	Gly	Ser	Phe	Asp	Tyr	Gly	Leu	Phe
				65					70					75
Gln	Ile	Asn	Ser	His	Tyr	Trp	Cys	Asn	Asp	Tyr	Lys	Ser	Tyr	Ser
				80					85					90
Glu	Asn	Leu	Cys	His	Val	Asp	Cys	Gln	Asp	Leu	Leu	Asn	Pro	Asn
				95					100					105
Leu	Leu	Ala	Gly	Ile	His	Cys	Ala	Lys	Arg	Ile	Val	Ser	Gly	Ala
				110					115					120
Arg	Gly	Met	Asn	Asn	Trp	Val	Glu	Trp	Arg	Leu	His	Cys	Ser	Gly
				125					130					135
Arg	Pro	Leu	Ser	Tyr	Trp	Leu	Thr	Gly	Cys	Arg	Leu	Arg		

```
<210> 341
<211> 23
<212> DNA
<213> Artificial
```

```
<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.
```

```
<400> 341
ccctccaagg atgacaaagg cgc 23
```

```
<210> 342
<211> 29
<212> DNA
<213> Artificial
```

<220>
<221> Artificial Sequence
<222> 1-29
<223> Synthetic construct.

```
<400> 342
ggtcagcagc tttcttgccc taaatcagg 29
```

```
<210> 343
<211> 24
<212> DNA
<213> Artificial
```

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

```
<400> 343
atctcaggcg gcatcctgtc agcc 24
```

```
<210> 344
<211> 24
<212> DNA
<213> Artificial
```

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

```
<400> 344
gtggatgcct gcaagaaggt tggg 24
```

```
<210> 345
<211> 45
<212> DNA
<213> Artificial
```


tatttcattg actgctggct gctta 2575

<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

Met	Leu	Leu	Arg	Lys	Arg	Tyr	Arg	His	Arg	Pro	Cys	Arg	Leu	Gln
1				5					10					15
Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Gly	Cys	Val	Leu	Met	Met	Val
				20					25					30
Ala	Met	Leu	His	Pro	Pro	His	His	Thr	Leu	His	Gln	Thr	Val	Thr
				35					40					45
Ala	Gln	Ala	Ser	Lys	His	Ser	Pro	Glu	Ala	Arg	Tyr	Arg	Leu	Asp
				50					55					60
Phe	Gly	Glu	Ser	Gln	Asp	Trp	Val	Leu	Glu	Ala	Glu	Asp	Glu	Gly
				65					70					75
Glu	Glu	Tyr	Ser	Pro	Leu	Glu	Gly	Leu	Pro	Pro	Phe	Ile	Ser	Leu
				80					85					90
Arg	Glu	Asp	Gln	Leu	Leu	Val	Ala	Val	Ala	Leu	Pro	Gln	Ala	Arg
				95					100					105
Arg	Asn	Gln	Ser	Gln	Gly	Arg	Arg	Gly	Gly	Ser	Tyr	Arg	Leu	Ile
				110					115					120
Lys	Gln	Pro	Arg	Arg	Gln	Asp	Lys	Glu	Ala	Pro	Lys	Arg	Asp	Trp
				125					130					135
Gly	Ala	Asp	Glu	Asp	Gly	Glu	Val	Ser	Glu	Glu	Glu	Glu	Leu	Thr
				140					145					150
Pro	Phe	Ser	Leu	Asp	Pro	Arg	Gly	Leu	Gln	Glu	Ala	Leu	Ser	Ala
				155					160					165
Arg	Ile	Pro	Leu	Gln	Arg	Ala	Leu	Pro	Glu	Val	Arg	His	Pro	Leu
				170					175					180
Cys	Leu	Gln	Gln	His	Pro	Gln	Asp	Ser	Leu	Pro	Thr	Ala	Ser	Val
				185					190					195
Ile	Leu	Cys	Phe	His	Asp	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr
				200					205					210
Val	His	Ser	Ile	Leu	Asp	Thr	Val	Pro	Arg	Ala	Phe	Leu	Lys	Glu
				215					220					225
Ile	Ile	Leu	Val	Asp	Asp	Leu	Ser	Gln	Gln	Gly	Gln	Leu	Lys	Ser
				230					235					240
Ala	Leu	Ser	Glu	Tyr	Val	Ala	Arg	Leu	Glu	Gly	Val	Lys	Leu	Leu
				245					250					255

Arg	Ser	Asn	Lys	Arg 260	Leu	Gly	Ala	Ile	Arg 265	Ala	Arg	Met	Leu	Gly 270
Ala	Thr	Arg	Ala	Thr 275	Gly	Asp	Val	Leu	Val 280	Phe	Met	Asp	Ala	His 285
Cys	Glu	Cys	His	Pro 290	Gly	Trp	Leu	Glu	Pro 295	Leu	Leu	Ser	Arg	Ile 300
Ala	Gly	Asp	Arg	Ser 305	Arg	Val	Val	Ser	Pro 310	Val	Ile	Asp	Val	Ile 315
Asp	Trp	Lys	Thr	Phe 320	Gln	Tyr	Tyr	Pro	Ser 325	Lys	Asp	Leu	Gln	Arg 330
Gly	Val	Leu	Asp	Trp 335	Lys	Leu	Asp	Phe	His 340	Trp	Glu	Pro	Leu	Pro 345
Glu	His	Val	Arg	Lys 350	Ala	Leu	Gln	Ser	Pro 355	Ile	Ser	Pro	Ile	Arg 360
Ser	Pro	Val	Val	Pro 365	Gly	Glu	Val	Val	Ala 370	Met	Asp	Arg	His	Tyr 375
Phe	Gln	Asn	Thr	Gly 380	Ala	Tyr	Asp	Ser	Leu 385	Met	Ser	Leu	Arg	Gly 390
Gly	Glu	Asn	Leu	Glu 395	Leu	Ser	Phe	Lys	Ala 400	Trp	Leu	Cys	Gly	Gly 405
Ser	Val	Glu	Ile	Leu 410	Pro	Cys	Ser	Arg	Val 415	Gly	His	Ile	Tyr	Gln 420
Asn	Gln	Asp	Ser	His 425	Ser	Pro	Leu	Asp	Gln 430	Glu	Ala	Thr	Leu	Arg 435
Asn	Arg	Val	Arg	Ile 440	Ala	Glu	Thr	Trp	Leu 445	Gly	Ser	Phe	Lys	Glu 450
Thr	Phe	Tyr	Lys	His 455	Ser	Pro	Glu	Ala	Phe 460	Ser	Leu	Ser	Lys	Ala 465
Glu	Lys	Pro	Asp	Cys 470	Met	Glu	Arg	Leu	Gln 475	Leu	Gln	Arg	Arg	Leu 480
Gly	Cys	Arg	Thr	Phe 485	His	Trp	Phe	Leu	Ala 490	Asn	Val	Tyr	Pro	Glu 495
Leu	Tyr	Pro	Ser	Glu 500	Pro	Arg	Pro	Ser	Phe 505	Ser	Gly	Lys	Leu	His 510
Asn	Thr	Gly	Leu	Gly 515	Leu	Cys	Ala	Asp	Cys 520	Gln	Ala	Glu	Gly	Asp 525
Ile	Leu	Gly	Cys	Pro 530	Met	Val	Leu	Ala	Pro 535	Cys	Ser	Asp	Ser	Arg 540
Gln	Gln	Gln	Tyr	Leu	Gln	His	Thr	Ser	Arg	Lys	Glu	Ile	His	Phe

				545					550					555
Gly	Ser	Pro	Gln	His 560	Leu	Cys	Phe	Ala	Val 565	Arg	Gln	Glu	Gln	Val 570
Ile	Leu	Gln	Asn	Cys 575	Thr	Glu	Glu	Gly	Leu 580	Ala	Ile	His	Gln	Gln 585
His	Trp	Asp	Phe	Gln 590	Glu	Asn	Gly	Met	Ile 595	Val	His	Ile	Leu	Ser 600
Gly	Lys	Cys	Met	Glu 605	Ala	Val	Val	Gln	Glu 610	Asn	Asn	Lys	Asp	Leu 615
Tyr	Leu	Arg	Pro	Cys 620	Asp	Gly	Lys	Ala	Arg 625	Gln	Gln	Trp	Arg	Phe 630
Asp	Gln	Ile	Asn	Ala 635	Val	Asp	Glu	Arg						

```
<210> 348
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 348
    ggagaggtgg tggccatgga cag 23

<210> 349
<211> 24
<212> DNA
<213> Artificial
```

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 349
ctgtcactgc aaggagccaa cacc 24

```
<210> 350
<211> 45
<212> DNA
<213> Artificial
```

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 350
tatgtcgcctg cgaagtggtg aaaacctcga actgtctttc aaggc 45

<210> 351
<211> 2524
<212> DNA
<213> Homo sapiens

<400> 351
cgccaagcat gcagtaaagg ctgaaaatct gggtcacagc tgaggaagac 50
ctcagacatg gagtccagga tgtggcctgc gctgctgctg tcccacctcc 100
tccctctctg gccactgctg ttgctgcccc tcccaccgcc tgctcagggc 150
tcttcatact cccctcgaac cccaccagcc ccagcccgcc ccccggtgtgc 200
caggggaggg ccctcggccc cacgtcatgt gtgcgtgtgg gagcgagcac 250
ctccaccaag ccgatctcct cgggtcccaa gatcacgtcg gcaagtcttg 300
cctggcactg cacccccagc caccocatca ggctttgagg agggggccgcc 350
ctcatcccaa taccctcggg ctatcgtgtg ggggtcccacc gtgtctcgag 400
aggatggagg ggaccccaac tctgccaatc ccggatttct ggactatggt 450
tttgagccc ctcatgggct cgcaacccca caccccaact cagactccat 500
gcgaggtgat ggagatgggc ttatccttgg agaggcacct gccaccctgc 550
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gtcacaatta ccatctccat catcattgtt ctctgggcca ctggcatcat 650
cttcaagttc tgctgggacc gcagccagaa gcgacgcaga ccctcagggc 700
agcaaggtgc cctgaggcag gaggagagcc agcagccact gacagacctg 750
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 caggttcttc cctccttctc actggttttt ccaccttcc ccttcccttc 2400
 ttccctggct cctaggtgtg gatatatatt tttgtattat ctctttcttc 2450
 ttcttggtgt gatcatcttg aattactgtg ggatgtaagt ttcaaaattt 2500
 tcaaataaag cctttgcaag ataa 2524

<210> 352

<211> 243

<212> PRT

<213> Homo sapiens

<400> 352

Met	Arg	Pro	Gln	Gly	Pro	Ala	Ala	Ser	Pro	Gln	Arg	Leu	Arg	Gly
1				5					10				15	

tccgggggttc tggccctgc ggtgtcaca gacgatgttc cacaggagcc 150
 cgtgcccacg ctgtggaacg agccggccga gctgccgtcg ggagaaggcc 200
 ccgtggagag caccagcccc ggccgggagc ccgtggacac cggccccca 250
 gccccaccg tcgcgccagg acccgaggac agcaccgcgc aggagcggct 300
 ggaccagggc ggccgggtcg tggggcccg cgctatcgcg gccatcgtga 350
 tcgccgccct gctggccacc tgcgtggtgc tggcgctcgt ggtcgtcgcg 400
 ctgagaaagt tttctgcctc ctgaagcgaa taaaggggcc gcgcccggcc 450
 gcggcgcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 354
 Met Ala Ser Cys Leu Ala Leu Arg Met Ala Leu Leu Leu Val Ser
 1 5 10 15
 Gly Val Leu Ala Pro Ala Val Leu Thr Asp Asp Val Pro Gln Glu
 20 25 30
 Pro Val Pro Thr Leu Trp Asn Glu Pro Ala Glu Leu Pro Ser Gly
 35 40 45
 Glu Gly Pro Val Glu Ser Thr Ser Pro Gly Arg Glu Pro Val Asp
 50 55 60
 Thr Gly Pro Pro Ala Pro Thr Val Ala Pro Gly Pro Glu Asp Ser
 65 70 75
 Thr Ala Gln Glu Arg Leu Asp Gln Gly Gly Gly Ser Leu Gly Pro
 80 85 90
 Gly Ala Ile Ala Ala Ile Val Ile Ala Ala Leu Leu Ala Thr Cys
 95 100 105
 Val Val Leu Ala Leu Val Val Val Ala Leu Arg Lys Phe Ser Ala
 110 115 120

Ser

<210> 355
 <211> 2134
 <212> DNA
 <213> Homo sapiens

<400> 355
 ggccgttggt tgggtgcgcgg ctgaagggtg tggcgcgagc agcgtcgttg 50
 gttggccggc ggcgggcccgg gacgggcatg gccctgctgc tgtgcctggt 100

140

145

150

Ser Pro Arg Gly Asp Leu Pro
155

<210> 357

<211> 1536

<212> DNA

<213> Homo sapiens

<400> 357

agcaggagca ggagagggac aatggaagct gccccgtcca ggttcatggt 50
cctcttattt ctctcacgt gtgagctggc tgcagaagtt gctgcagaag 100
ttgagaaatc ctcatggtt cctgggtgctg cccaggaacc cacgtggctc 150
acagatgtcc cagctgccat ggaattcatt gctgccactg aggtggctgt 200
cataggcttc ttccaggatt tagaaatacc agcagtgcc atactccata 250
gcatgggtgca aaaattccca ggcgtgtcat ttgggatcag cactgattct 300
gaggttctga cactactaaa catcactggg aacaccatct gcctctttcg 350
cctggtagac aatgaacaac tgaatttaga ggacgaagac attgaaagca 400
ttgatgccac caaattgagc cgtttcattg agatcaacag cctccacatg 450
gtgacagagt acaaccctgt gactgtgatt gggttattca acagcgtaat 500
tcagattcat ctctctctga taatgaacaa ggcctcccca gagtatgaag 550
agaacatgca cagataccag aaggcagcca agctcttcca ggggaagatt 600
ctctttattc tggtaggacag tggtagaaa gaaaatggga aggtgatatc 650
atctttcaaa ctaaaggagt ctcaactgcc agctttggca atttaccaga 700
ctctagatga cgagtgggat aactgccc cagcagaagt ttccgtagag 750
catgtgcaaa acttttgtga tggattccta agtggaat tgttgaaaga 800
aaatcgtgaa tcagaaggaa agactccaaa ggtggaactc tgacttctcc 850
ttggaactac atatggccaa gtatctactt tatgcaaagt aaaaaggcac 900
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acacacacac gcacgtgcac acacgcacgc acgcgtgcac acacacacgc 1000
gcacacacac acacacacag agcttcattt cctgtcttaa aatctcgttt 1050
tctcttcttc cttcttttaa atttcatatc ctcaactcct atccaatttc 1100
cttcttatcg tgcattcata ctctgtaagc ccatctgtaa cacacctaga 1150
tcaaggcttt aagagactca ctgtgatgcc totatgaaag agaggcattc 1200

ctagagaaag attgttccaa tttgtcattt aatatcaagt ttgtatactg 1250
cacatgactt acacacaaca tagttcctgc tcttttaagg ttacctaagg 1300
gttgaaactc taccttcttt cataagcaca tgtccgtctc tgactcagga 1350
tcaaaaaacca aaggatgggt ttaaacacct ttgtgaaatt gtctttttgc 1400
cagaagttaa aggctgtctc caagtccctg aactcagcag aaatagacca 1450
tgtgaaaact ccatgcttgg ttagcatctc caactcccta tgtaaataca 1500
caacctgcat aataaataaa aggcaatcat gttata 1536

<210> 358

<211> 273

<212> PRT

<213> Homo sapiens

<400> 358

Met	Glu	Ala	Ala	Pro	Ser	Arg	Phe	Met	Phe	Leu	Leu	Phe	Leu	Leu	1	5	10	15
Thr	Cys	Glu	Leu	Ala	Ala	Glu	Val	Ala	Ala	Glu	Val	Glu	Lys	Ser	20	25	30	
Ser	Asp	Gly	Pro	Gly	Ala	Ala	Gln	Glu	Pro	Thr	Trp	Leu	Thr	Asp	35	40	45	
Val	Pro	Ala	Ala	Met	Glu	Phe	Ile	Ala	Ala	Thr	Glu	Val	Ala	Val	50	55	60	
Ile	Gly	Phe	Phe	Gln	Asp	Leu	Glu	Ile	Pro	Ala	Val	Pro	Ile	Leu	65	70	75	
His	Ser	Met	Val	Gln	Lys	Phe	Pro	Gly	Val	Ser	Phe	Gly	Ile	Ser	80	85	90	
Thr	Asp	Ser	Glu	Val	Leu	Thr	His	Tyr	Asn	Ile	Thr	Gly	Asn	Thr	95	100	105	
Ile	Cys	Leu	Phe	Arg	Leu	Val	Asp	Asn	Glu	Gln	Leu	Asn	Leu	Glu	110	115	120	
Asp	Glu	Asp	Ile	Glu	Ser	Ile	Asp	Ala	Thr	Lys	Leu	Ser	Arg	Phe	125	130	135	
Ile	Glu	Ile	Asn	Ser	Leu	His	Met	Val	Thr	Glu	Tyr	Asn	Pro	Val	140	145	150	
Thr	Val	Ile	Gly	Leu	Phe	Asn	Ser	Val	Ile	Gln	Ile	His	Leu	Leu	155	160	165	
Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr	Glu	Glu	Asn	Met	His	170	175	180	
Arg	Tyr	Gln	Lys	Ala	Ala	Lys	Leu	Phe	Gln	Gly	Lys	Ile	Leu	Phe	185	190	195	

Ile	Leu	Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser
				200					205					210
Phe	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala	Ile	Tyr
				215					220					225
Gln	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu	Val
				230					235					240
Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu	Ser	Gly
				245					250					255
Lys	Leu	Leu	Lys	Glu	Asn	Arg	Glu	Ser	Glu	Gly	Lys	Thr	Pro	Lys
				260					265					270

Val Glu Leu

<210> 359
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 359
 ccagcagtgc ccatactcca tagc 24

<210> 360
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 360
 tgacgagtgg gatacactgc 20

<210> 361
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 361
 gctctacgga aacttctgct gtgg 24

<210> 362

<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 362
attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363
<211> 1777
<212> DNA
<213> Homo sapiens

<400> 363
ggagagccgc ggctgggacc ggagtgggga gcgcggcgtg gaggtgccac 50
ccggcgcggg tggcggagag atcagaagcc tcttcccca gccgagccaa 100
cctcagcggg gaccggggt cagggacgcg gcggcggcgg cggcgactgc 150
agtggctgga cgatggcagc gtccgccgga gccggggcgg tgattgcagc 200
cccagacagc cggcgcctggc tgtggctcgg gctggcggcg gcgcttgggc 250
tcttgacagc tggagtatca gccttggaag tatatacgcc aaaagaaatc 300
ttcgtggcaa atggtacaca agggaagctg acctgcaagt tcaagtctac 350
tagtacgact ggcgggttga cctcagcttc ctggagcttc cagccagagg 400
gggccgacac tactgtgtcg tttttccact actcccaagg gcaagtgtac 450
cttgggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500
tgacaagaaa gatgcatcaa tcaacataga aaatatgcag ttatacaca 550
atggcaccta tatctgtgat gtcaaaaacc ctctgacat cgttgtccag 600
cctggacaca ttaggctcta tgtcgtagaa aaagagaatt tgctgtgtt 650
tccagtttgg gtagtggtgg gcatagttac tgctgtggtc ctaggtctca 700
ctctgctcat cagcatgatt ctggetgtcc tctatagaag gaaaaactct 750
aaacgggatt aactggctg cagtacatca gagagtttgt caccagttaa 800
gcaggctcct cggaagtccc cctccgacac tgagggtctt gtaaagagtc 850
tgcttcttgg atctcaccag ggcccagtca tatatgcaca gttagaccac 900
tccggcggac atcacagtga caagattaac aagtcagagt ctgtggtgta 950
tgcggatatc cgaaagaatt aagagaatac ctagaacata tcctcagcaa 1000

Arg Ile Ser Trp	Ala Gly Asp Leu	Asp Lys Lys Asp	Ala Ser Ile
110		115	120
Asn Ile Glu Asn	Met Gln Phe Ile	His Asn Gly Thr	Tyr Ile Cys
125		130	135
Asp Val Lys Asn	Pro Pro Asp Ile	Val Val Gln Pro	Gly His Ile
140		145	150
Arg Leu Tyr Val	Val Glu Lys Glu	Asn Leu Pro Val	Phe Pro Val
155		160	165
Trp Val Val Val	Gly Ile Val Thr	Ala Val Val Leu	Gly Leu Thr
170		175	180
Leu Leu Ile Ser	Met Ile Leu Ala	Val Leu Tyr Arg	Arg Lys Asn
185		190	195
Ser Lys Arg Asp	Tyr Thr Gly Cys	Ser Thr Ser Glu	Ser Leu Ser
200		205	210
Pro Val Lys Gln	Ala Pro Arg Lys	Ser Pro Ser Asp	Thr Glu Gly
215		220	225
Leu Val Lys Ser	Leu Pro Ser Gly	Ser His Gln Gly	Pro Val Ile
230		235	240
Tyr Ala Gln Leu	Asp His Ser Gly	Gly His His Ser	Asp Lys Ile
245		250	255
Asn Lys Ser Glu	Ser Val Val Tyr	Ala Asp Ile Arg	Lys Asn
260		265	

<210> 365
 <211> 1321
 <212> DNA
 <213> Homo sapiens

<400> 365
 gccggctgtg cagagacgcc atgtaccggc tctgtcagc agtgactgcc 50
 cgggctgccg cccccggggg cttggcctca agctgcggac gacgcggggg 100
 ccatcagcgc gccgggctgc cgcctctcgg ccacggctgg gtcggggggc 150
 tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200
 aggggcgcg ccccggcgca gtcccccgcg gcccccgacc ctgaggcgctc 250
 gcctctggcc gagccgccac aggagcagtc cctcgccccg tggctctccgc 300
 agaccccggc gccgccctgc tccaggtgct tcgccagagc catcgagagc 350
 agccgcgacc tgctgcacag gatcaaggat gaggtgggcg caccgggcat 400
 agtggttga gtttctgtag atggaaaaga agtctggtca gaaggtttag 450
 gttatgctga tgttgagaac cgtgtacat gtaaaccaga gacagttatg 500

<211> 30
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-30
<223> Synthetic construct.

<400> 367
tggaagaa gtctggtcag aaggttagg 30

<210> 368
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 368
catttggtt cattctctg ctctg 25

<210> 369
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-28
<223> Synthetic construct.

<400> 369
aaaacctcag aacaactcat ttgcacc 28

<210> 370
<211> 41
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-41
<223> Synthetic construct.

<400> 370
gtctcaccat ggttgctctt gccaaattgt gggaagcagg g 41

<210> 371
<211> 1150
<212> DNA
<213> Homo sapiens

<400> 371
gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

gaattcggct cgaggctggt gggaagaagc cgagatggcg gcagccagcg 100
ctggggcaac ccggctgctc ctgctcttgc tgatggcggt agcagcgccc 150
agtcgagccc ggggcagcgg ctgccgggcc gggactggtg cgcgaggggc 200
tggggcgga ggtcgagagg gcgaggcctg tggcacggtg gggctgctgc 250
tggagcactc atttgagatc gatgacagt ccaacttccg gaagcggggc 300
tcactgctct ggaaccagca ggatggtacc ttgtccctgt cacagcgcca 350
gctcagcgag gaggagcggg gccgactccg ggatgtggca gccctgaatg 400
gcctgtaccg ggtccggatc ccaaggcgac ccggggccct ggatggcctg 450
gaagctggtg gctatgtctc ctcccttgtc cctgcgtgct ccctggtgga 500
gtcgcacctg tcggaccagc tgaccctgca cgtggatgtg gccggcaacg 550
tgggtgggctg gtcggtggtg acgcaccccg ggggctgccg gggccatgag 600
gtggaggacg tggacctgga gctgttcaac acctcggtgc agctgcagcc 650
gcccaccaca gcccaggcc ctgagacggc ggccttcatt gagcgccctg 700
agatggaaca ggcccagaag gccaagaacc cccaggagca gaagtccttc 750
ttcgccaaat actggatgta catcattccc gtctgctctg tcctcatgat 800
gtcaggagcg ccagacaccg ggggccaggg tgggggtggg ggtgggggtg 850
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ttaaaaacat cgacgataca ttgaaatgtg tgaacgtttt gaaaagctac 950
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tacaagcttg attgaaattc actgctcact tgatacgtta ttcagaaacc 1050
caaggaatgg ctgtcccat cctcatgtgg ctgtgtggag ctgagctgtg 1100
ttgtgtggca gtttattaaa ctgtcccca gatcgacacg caaaaaaaaa 1150

<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met	Ala	Ala	Ala	Ser	Ala	Gly	Ala	Thr	Arg	Leu	Leu	Leu	Leu	Leu
1				5					10					15

Leu	Met	Ala	Val	Ala	Ala	Pro	Ser	Arg	Ala	Arg	Gly	Ser	Gly	Cys
			20						25					30

Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu
			35						40					45

Gly	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe	
				50					55					60	
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu	
				65					70					75	
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu	
				80					85					90	
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn	
				95					100					105	
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp	
				110					115					120	
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys	
				125					130					135	
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val	
				140					145					150	
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro	
				155					160					165	
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu	
				170					175					180	
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly	
				185					190					195	
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala	
				200					205					210	
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys	
				215					220					225	
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser	
				230					235					240	
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly	Gly	Gly	Gly	Gly	Gly	Gly	
				245					250					255	
Gly	Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu		
				260					265						

<210> 373
 <211> 1706
 <212> DNA
 <213> Homo sapiens

<400> 373
 ggagcgctgc tggaaacccga gccggagccg gagccacagc ggggagggtg 50
 gcctggcggc ctggagccgg acgtgtccgg ggcgtccccg cagaccgggg 100
 cagcaggctcg tccggggggcc caccatgctg gtgactgcct accttgcttt 150
 tgtaggcctc ctggcctcct gcctggggct ggaactgtca agatgccggg 200

ctaaaccccc tgaaggggcc tgcagcaatc cctccttcct tcggtttcaa 250
ctggactttct atcaggtcta cttcctggcc ctggcagctg attggcttca 300
ggccccctac ctctataaac tctaccagca ttactacttc ctggaaggctc 350
aaattgccat cctctatgtc tgtggccttg cctctacagt cctctttggc 400
ctagtggcct cctcccttgt ggattggctg ggtcgcaaga attcttgtgt 450
cctctttctcc ctgacttact cactatgctg ctttaaccaa ctctctcaag 500
actactttgt gctgctagtg gggcgagcac ttggtgggct gtccacagcc 550
ctgctctttct cagccttcga ggccctggat atccatgagc acgtggaacg 600
gcatgacttc cctgctgagt ggatcccagc tacctttgct cgagctgcct 650
tctggaacca tgtgctggct gtagtggcag gtgtggcagc tgaggctgta 700
gccagctgga tagggctggg gcctgtagcg ccctttgtgg ctgccatccc 750
tctcctggct ctggcagggg ccttggccct tcgaaactgg ggggagaact 800
atgaccggca gcgtgccttc tcaaggacct gtgctggagg cctgcgctgc 850
ctcctgtcgg accgcgcgt gctgctgctg ggcaccatac aagctctatt 900
tgagagtgtc atcttcatct ttgtcttcct ctggacacct gtgctggacc 950
cacacggggc ccctctgggc attatcttct ccagcttcat ggcagccagc 1000
ctgcttggct cttccctgta ccgtatcgcc acctccaaga ggtaccacct 1050
tcagcccatg cacctgctgt cccttgctgt gctcatcgtc gtcttctctc 1100
tcttcatgtt gactttctct accagcccag gccaggagag tccggtggag 1150
tccttcatag cctttctact tattgagttg gcttgtggat tatactttcc 1200
cagcatgagc ttcctacgga gaaaggatgat ccctgagaca gagcaggctg 1250
gtgtactcaa ctggttcocg gtacctctgc actcactggc ttgcctaggg 1300
ctccttgtcc tccatgacag tgatcgaaaa acaggcactc ggaatatgtt 1350
cagcatttgc tctgctgtca tggatgatggc tctgctggca gtggtgggac 1400
tcttcaccgt ggtaaggcat gatgctgagc tgcgggtacc ttcacctact 1450
gaggagccct atgcccctga gctgtaacct cactccagga caagatagct 1500
gggacagact cttgaattcc agctatccgg gattgtacag atctctctgt 1550
gactgacttt gtgactgtcc tgtggtttct cctgccattg ctttgtgttt 1600
gggaggacat gatgggggtg atggactgga aagaaggctg caaaagttcc 1650

ctctgtgtta ctccattta gaaaataaac actttttaaat gatcaaaaaa 1700

aaaaaa 1706

<210> 374

<211> 450

<212> PRT

<213> Homo sapiens

<400> 374

Met	Leu	Val	Thr	Ala	Tyr	Leu	Ala	Phe	Val	Gly	Leu	Leu	Ala	Ser
1				5					10					15
Cys	Leu	Gly	Leu	Glu	Leu	Ser	Arg	Cys	Arg	Ala	Lys	Pro	Pro	Gly
				20					25					30
Arg	Ala	Cys	Ser	Asn	Pro	Ser	Phe	Leu	Arg	Phe	Gln	Leu	Asp	Phe
				35					40					45
Tyr	Gln	Val	Tyr	Phe	Leu	Ala	Leu	Ala	Ala	Asp	Trp	Leu	Gln	Ala
				50					55					60
Pro	Tyr	Leu	Tyr	Lys	Leu	Tyr	Gln	His	Tyr	Tyr	Phe	Leu	Glu	Gly
				65					70					75
Gln	Ile	Ala	Ile	Leu	Tyr	Val	Cys	Gly	Leu	Ala	Ser	Thr	Val	Leu
				80					85					90
Phe	Gly	Leu	Val	Ala	Ser	Ser	Leu	Val	Asp	Trp	Leu	Gly	Arg	Lys
				95					100					105
Asn	Ser	Cys	Val	Leu	Phe	Ser	Leu	Thr	Tyr	Ser	Leu	Cys	Cys	Leu
				110					115					120
Thr	Lys	Leu	Ser	Gln	Asp	Tyr	Phe	Val	Leu	Leu	Val	Gly	Arg	Ala
				125					130					135
Leu	Gly	Gly	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Ser	Ala	Phe	Glu	Ala
				140					145					150
Trp	Tyr	Ile	His	Glu	His	Val	Glu	Arg	His	Asp	Phe	Pro	Ala	Glu
				155					160					165
Trp	Ile	Pro	Ala	Thr	Phe	Ala	Arg	Ala	Ala	Phe	Trp	Asn	His	Val
				170					175					180
Leu	Ala	Val	Val	Ala	Gly	Val	Ala	Ala	Glu	Ala	Val	Ala	Ser	Trp
				185					190					195
Ile	Gly	Leu	Gly	Pro	Val	Ala	Pro	Phe	Val	Ala	Ala	Ile	Pro	Leu
				200					205					210
Leu	Ala	Leu	Ala	Gly	Ala	Leu	Ala	Leu	Arg	Asn	Trp	Gly	Glu	Asn
				215					220					225
Tyr	Asp	Arg	Gln	Arg	Ala	Phe	Ser	Arg	Thr	Cys	Ala	Gly	Gly	Leu
				230					235					240

Glu Arg Gly Gly Cys Ser Phe Leu Ser Lys Thr Arg Val Val Gln
95 100 105

Glu His Gly Gly Arg Ala Val Ile Ile Ser Asp Asn Ala Val Asp
110 115 120

Asn Asp Ser Phe Tyr Val Glu Met Ile Gln Asp Ser Thr Gln Arg
125 130 135

Thr Ala Asp Ile Pro Ala Leu Phe Leu Leu Gly Arg Asp Gly Tyr
140 145 150

Met Ile Arg Arg Ser Leu Glu Gln His Gly Leu Pro Trp Ala Ile
155 160 165

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Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro Thr Phe Glu Leu
      170                      175                      180

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Leu Gln Pro Pro Trp Thr Phe Trp
185

<210> 377

<211> 496

<212> DNA

<213> Artificial

 $\langle 220 \rangle$

<221> unsure

<222> 396

<223> unknown base

<400> 377

tctgcootcca ctgctctgtg ctgggatcat ggaacttgca ctgctgtgtg 50

ggctggtggt gatggctggt gtgattccaa tccagggcgg gatcctgaac 100

ctgaacaaga tgggtcaagca agtgactggg aaaatgccca tcctctccta 150

ctggccctac ggctgtcact gcggactagg tggcagaggc caacccaaaag 200

atgccacgga ctggtgctgc cagacccatg actgctgcta tgaccacctg 250

aagacccagg ggtgcggcat ctacaaggac aacaacaaaa gcagcatata 300

ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350

tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 496

<210> 378

<211> 116

<212> PRT

<213> Homo sapiens

<400> 378

Met	Glu	Leu	Ala	Leu	Leu	Cys	Gly	Leu	Val	Val	Met	Ala	Gly	Val	1	5	10	15
Ile	Pro	Ile	Gln	Gly	Gly	Ile	Leu	Asn	Leu	Asn	Lys	Met	Val	Lys	20	25	30	
Gln	Val	Thr	Gly	Lys	Met	Pro	Ile	Leu	Ser	Tyr	Trp	Pro	Tyr	Gly	35	40	45	
Cys	His	Cys	Gly	Leu	Gly	Gly	Arg	Gly	Gln	Pro	Lys	Asp	Ala	Thr	50	55	60	
Asp	Trp	Cys	Cys	Gln	Thr	His	Asp	Cys	Cys	Tyr	Asp	His	Leu	Lys	65	70	75	
Thr	Gln	Gly	Cys	Gly	Ile	Tyr	Lys	Asp	Asn	Asn	Lys	Ser	Ser	Ile	80	85	90	
His	Cys	Met	Asp	Leu	Ser	Gln	Arg	Tyr	Cys	Leu	Met	Ala	Val	Phe	95	100	105	
Asn	Val	Ile	Tyr	Leu	Glu	Asn	Glu	Asp	Ser	Glu	110	115						

<210> 379
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 379
 ctgcctccac tgctctgtgc tggg 24

<210> 380
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 380
 cagagcagtg gatgttcccc tggg 24

<210> 381
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45

atctcagaaa ttacaggaga taccctcaag tataatctgct ggttgcttag 700
 gtttgtccct tcgctataac agccttcaaa aacttaagta taatcaattt 750
 aaagggctca accagctcac ctggctatac cttgaccata accatatcag 800
 caatattgac gaaaatgctt ttaatggaat acgcagactc aaagagctga 850
 ttcttagttc caatagaatc tcctattttc ttaacaatac cttcagacct 900
 gtgacaaatt tacggaactt ggatctgtcc tataatcagc tgcattctct 950
 gggatctgaa cagtttcggg gcttgcgga gctgctgagt ttacatttac 1000
 ggtctaactc cctgagaacc atccctgtgc gaatattcca agactgccgc 1050
 aacctggaac ttttgacct gggatataac cggatccgaa gtttagccag 1100
 gaatgtcttt gctggcatga tcagactcaa agaacttcac ctggagcaca 1150
 atcaattttc caagctcaac ctggcccttt ttccaagggt ggtcagcctt 1200
 cagaaccttt acttgcatg gaataaaatc agtgtcatag gacagaccat 1250
 gtcttgacc tggagctcct taaaaaggct tgatttatca ggcaatgaga 1300
 tcgaagcttt cagtggacc agtggtttcc agtgtgtccc gaatctgcag 1350
 cgctcaacc tggattccaa caagctcaca ttattggtc aagagatttt 1400
 ggattcttgg atatccctca atgacatcag tcttgctggg aatatatggg 1450
 aatgcagcag aaatatttgc tcccttgtaa actggctgaa aagttttaaa 1500
 ggtctaaggg agaatacaat tatctgtgcc agtcccaaag agctgcaagg 1550
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 ctacagagag gtttgatctg gccagggctc tcccaaagcc gacgtttaag 1650
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 aaagacagtc cctaaagcaa atgactccca gcaccagga attttatgta 1950
 gattataaac ccaccaacac ggagaccagc gagatgctgc tgaatgggac 2000
 gggacctgc acctataaca aatcgggctc caggagagtgt gaggtatgaa 2050
 ccattgtgat aaaaagagct cttaaaagct gggaaataag tgggtgttta 2100

ttgaactctg gtgactatca agggaacgcg atgccccccc tccccttccc 2150
 tctccctctc acttttggtgg caagatcctt ccttgtccgt tttagtgcac 2200
 tcataatact ggtcattttc ctctcatata taatcaaccc attgaaattt 2250
 aaataccaca atcaatgtga agcttgaact ccggtttaat ataataccta 2300
 ttgtataaga ccctttactg attccattaa tgtcgcattt gttttaagat 2350
 aaaacttctt tcataggtaa aaaaaaaaaa 2379

<210> 385
 <211> 513
 <212> PRT
 <213> Homo sapiens

<400> 385

Met	Gly	Phe	Asn	Val	Ile	Arg	Leu	Leu	Ser	Gly	Ser	Ala	Val	Ala	1	5	10	15
Leu	Val	Ile	Ala	Pro	Thr	Val	Leu	Leu	Thr	Met	Leu	Ser	Ser	Ala	20	25	30	
Glu	Arg	Gly	Cys	Pro	Lys	Gly	Cys	Arg	Cys	Glu	Gly	Lys	Met	Val	35	40	45	
Tyr	Cys	Glu	Ser	Gln	Lys	Leu	Gln	Glu	Ile	Pro	Ser	Ser	Ile	Ser	50	55	60	
Ala	Gly	Cys	Leu	Gly	Leu	Ser	Leu	Arg	Tyr	Asn	Ser	Leu	Gln	Lys	65	70	75	
Leu	Lys	Tyr	Asn	Gln	Phe	Lys	Gly	Leu	Asn	Gln	Leu	Thr	Trp	Leu	80	85	90	
Tyr	Leu	Asp	His	Asn	His	Ile	Ser	Asn	Ile	Asp	Glu	Asn	Ala	Phe	95	100	105	
Asn	Gly	Ile	Arg	Arg	Leu	Lys	Glu	Leu	Ile	Leu	Ser	Ser	Asn	Arg	110	115	120	
Ile	Ser	Tyr	Phe	Leu	Asn	Asn	Thr	Phe	Arg	Pro	Val	Thr	Asn	Leu	125	130	135	
Arg	Asn	Leu	Asp	Leu	Ser	Tyr	Asn	Gln	Leu	His	Ser	Leu	Gly	Ser	140	145	150	
Glu	Gln	Phe	Arg	Gly	Leu	Arg	Lys	Leu	Leu	Ser	Leu	His	Leu	Arg	155	160	165	
Ser	Asn	Ser	Leu	Arg	Thr	Ile	Pro	Val	Arg	Ile	Phe	Gln	Asp	Cys	170	175	180	
Arg	Asn	Leu	Glu	Leu	Leu	Asp	Leu	Gly	Tyr	Asn	Arg	Ile	Arg	Ser	185	190	195	
Leu	Ala	Arg	Asn	Val	Phe	Ala	Gly	Met	Ile	Arg	Leu	Lys	Glu	Leu				

200	205	210
His Leu Glu His Asn Gln Phe Ser Lys	Leu Asn Leu Ala Leu Phe	
215	220	225
Pro Arg Leu Val Ser Leu Gln Asn Leu	Tyr Leu Gln Trp Asn Lys	
230	235	240
Ile Ser Val Ile Gly Gln Thr Met Ser	Trp Thr Trp Ser Ser Leu	
245	250	255
Gln Arg Leu Asp Leu Ser Gly Asn Glu	Ile Glu Ala Phe Ser Gly	
260	265	270
Pro Ser Val Phe Gln Cys Val Pro Asn	Leu Gln Arg Leu Asn Leu	
275	280	285
Asp Ser Asn Lys Leu Thr Phe Ile Gly	Gln Glu Ile Leu Asp Ser	
290	295	300
Trp Ile Ser Leu Asn Asp Ile Ser Leu	Ala Gly Asn Ile Trp Glu	
305	310	315
Cys Ser Arg Asn Ile Cys Ser Leu Val	Asn Trp Leu Lys Ser Phe	
320	325	330
Lys Gly Leu Arg Glu Asn Thr Ile Ile	Cys Ala Ser Pro Lys Glu	
335	340	345
Leu Gln Gly Val Asn Val Ile Asp Ala	Val Lys Asn Tyr Ser Ile	
350	355	360
Cys Gly Lys Ser Thr Thr Glu Arg Phe	Asp Leu Ala Arg Ala Leu	
365	370	375
Pro Lys Pro Thr Phe Lys Pro Lys Leu	Pro Arg Pro Lys His Glu	
380	385	390
Ser Lys Pro Pro Leu Pro Pro Thr Val	Gly Ala Thr Glu Pro Gly	
395	400	405
Pro Glu Thr Asp Ala Asp Ala Glu His	Ile Ser Phe His Lys Ile	
410	415	420
Ile Ala Gly Ser Val Ala Leu Phe Leu	Ser Val Leu Val Ile Leu	
425	430	435
Leu Val Ile Tyr Val Ser Trp Lys Arg	Tyr Pro Ala Ser Met Lys	
440	445	450
Gln Leu Gln Gln Arg Ser Leu Met Arg	Arg His Arg Lys Lys Lys	
455	460	465
Arg Gln Ser Leu Lys Gln Met Thr Pro	Ser Thr Gln Glu Phe Tyr	
470	475	480
Val Asp Tyr Lys Pro Thr Asn Thr Glu	Thr Ser Glu Met Leu Leu	
485	490	495

Asn	Gly	Thr	Gly	Pro	Cys	Thr	Tyr	Asn	Lys	Ser	Gly	Ser	Arg	Glu
				500					505					510

Cys Glu Val

<210> 386
 <211> 24
 <212> DNA
 <213> Artificial

<220>
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 <222> 1-24
 <223> Synthetic construct.

<400> 386
 ctgggatctg aacagtttcg gggc 24

<210> 387
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 387
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<210> 388
 <211> 48
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-48
 <223> Synthetic construct.

<400> 388
 gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389
 <211> 1449
 <212> DNA
 <213> Homo sapiens

<400> 389
 agttctgaga aagaaggaaa taaacacagg caccaaacca ctatcctaag 50
 ttgactgtcc tttaaatatg tcaagatcca gacttttcag tgtcacctca 100
 gcgatctcaa cgatagggat cttgtgtttg ccgctattcc agttggtgct 150
 ctcggaccta ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 393
ccagttggtg ctctcggacc taccatgcga agaagatgaa atgtgtg 47

<210> 394
<211> 2340
<212> DNA
<213> Homo sapiens

<400> 394
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accacccggc gtttctccag ctcgatctgg aggctgcttc gccagtgtgg 100
gacgcagctg acgcccgtt attagctctc gctgcgtcgc cccggctcag 150
aagctccgtg gcggcggcga ccgtgacgag aagcccacgg ccagctcagt 200
tctcttctac tttgggagag agagaaagtc agatgccctt tttaaactcc 250
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cttgctgaag atgaagaata tacaatattg aggatatttt tttctttttt 350
ttttcaagtc ttgatttgtg gcttacctca agttaccatt tttcagtcaa 400
gtctgtttgt ttgcttcttc agaaatgttt tttacaatct caagaaaaaa 450
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atgacatgcc attgtgggga ggaagcaatg aagaaataca gccagattct 800
 gagtcacttt gaaaagctgg aacctcaggc agcagttgtg aaggctttgg 850
 gggaactaga cattcttctg caatggatgg aggagacaga ataggaggaa 900
 agtgatgctg ctgctaagaa tattcgaggt caagagctcc agtcttcaat 950
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 atttttgtaa tatctttctg ctattggata tttttattag ttaatatatt 1150
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 gtatttttat acagtaaaaa aaaaaaacct tgtaaattct agaagagtgg 1300
 ctaggggggt tattcatttg tattcaacta aggacatatt tactcatgct 1350
 gatgctctgt gagatatttg aaattgaacc aatgactact taggatgggt 1400
 tgtggaataa gttttgatgt ggaattgcac atctacctta caattactga 1450
 ccatccccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500
 aatcctacac ggccagcatg tatttctaca aataaagttt tctttgcata 1550
 ccaaaaaaaaa aaaaaaaaaa a 1571

<210> 402

<211> 261

<212> PRT

<213> Homo sapiens

<400> 402

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Ser	Phe	Ser	Ile	Tyr	Ser	Leu	Gln	Val	Pro	Ala	Val	Pro	Gly	Leu
				20					25					30
Thr	Cys	Trp	Ala	Leu	Thr	Ala	Glu	Pro	Gly	Trp	Gly	Gln	Asn	Lys
				35					40					45
Gly	Ala	Thr	Thr	Cys	Ala	Thr	Asn	Ser	His	Ser	Asp	Ser	Glu	Leu
				50					55					60
Arg	Pro	Glu	Ile	Phe	Ser	Ser	Arg	Glu	Ala	Trp	Gln	Phe	Phe	Leu
				65					70					75
Leu	Leu	Trp	Ser	Pro	Asp	Phe	Arg	Pro	Lys	Met	Lys	Ala	Ser	Ser
				80					85					90

Ser Asn Ala Gln Val Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu
80 85 90

Gly Arg Thr Gly Ala Arg Val Trp Leu Phe Ile Gly Phe Met Leu
95 100 105

Met Phe Gly Ser Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Ala
110 115 120

Tyr Val Thr Gln Asn Thr Asp Val Tyr Pro Gly Leu Ala Val Phe
125 130 135

Phe Gln Asn Ala Leu Ile Phe Phe Ser Thr Leu Ile Tyr Lys Phe
140 145 150

Gly Arg Thr Glu Glu Leu Trp Thr
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<210> 411

<211> 20

<212> DNA

<213> Artificial

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<221> Artificial Sequence

<222> 1-20

<223> Synthetic construct.

<400> 411

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<210> 412

<211> 20

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-20

<223> Synthetic construct.

<400> 412

ccaaactcga gcacctgttc 20

<210> 413

<211> 40

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-40

<223> Synthetic construct.

<400> 413

atggcaggct tcctagataa ttttcgttgg ccagaatgtg 40

<210> 414

<211> 1337
<212> DNA
<213> Homo sapiens

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actgcatcta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150
gggaggtggg actgtcagaa gctggcccag ggtggtggtc agctgggtca 200
gggacctacg gcacctgctg gaccacctcg ccttctccat cgaagcaggg 250
aagtgggagc ctcgagccct cgggtggaag ctgaccccaa gccacccttc 300
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tttgccatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400
catgaaaacc atccgtctgc cacgctgggt ggcagcctcg cccaccaagg 450
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aactactttg cgtttaaaat ctgcagtggg gccgccaacg tcgtgggccc 550
tactatgtgc tttgaagacc gcatgatcat gagtcctgtg aaaaacaatg 600
tgggcagagg cctaaacatc gccctggtga atggaaccac gggagctgtg 650
ctgggacaga aggcatttga catgtactct ggagatgtta tgcacctagt 700
gaaattcctt aaagaaattc cgggggggtgc actggtgctg gtggcctcct 750
acgacgatcc agggaccaaa atgaacgatg aaagcaggaa actcttctct 800
gacttgggga gttcctacgc aaaacaactg ggcttccggg acagctgggt 850
cttcatagga gccaaagacc tcaggggtaa aagccccttt gagcagttct 900
taaagaacag cccagacaca aacaaatacg agggatggcc agagctgctg 950
gagatggagg gctgcatgcc cccgaagcca ttttaggggtg gctgtggctc 1000
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tcccacagca catcctaccc ggaagaccag cctcagaggg tccttctgga 1200
accagctgtc tgtggagaga atggggtgct ttcgtcaggg actgctgacg 1250
gctggtcctg aggaaggaca aactgccag acttgagccc aattaaattt 1300
tatttttgcg ggttttgaaa aaaaaaaaaa aaaaaaa 1337

<210> 415
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 415
 Met Arg Val Ser Gly Val Leu Arg Leu Leu Ala Leu Ile Phe Ala
 1 5 10 15
 Ile Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser
 20 25 30
 Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr
 35 40 45
 Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro
 50 55 60
 Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala
 65 70 75
 Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met
 80 85 90
 Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu
 95 100 105
 Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp
 110 115 120
 Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu
 125 130 135
 Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro
 140 145 150
 Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu
 155 160 165
 Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val
 170 175 180
 Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln
 185 190 195
 Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro
 200 205 210
 Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe
 215 220

<210> 416
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence

<222> 1-21
<223> Synthetic construct.

<400> 416
gccatagtcg cgacatggat g 21

<210> 417
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 417
ggatggccag agctgctg 18

<210> 418
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-26
<223> Synthetic construct.

<400> 418
aaagtacaag tgtggcctca tcaagc 26

<210> 419
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 419
tctgactcct aagtcaggca ggag 24

<210> 420
<211> 24
<212> DNA
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<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 420
attctctcca cagacagctg gttc 24

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				95					100					105
Ala	Gln	Leu	His	Leu	His	Trp	Gly	Gln	Lys	Gly	Ser	Pro	Gly	Gly
				110					115					120
Ser	Glu	His	Gln	Ile	Asn	Ser	Glu	Ala	Thr	Phe	Ala	Glu	Leu	His
				125					130					135
Ile	Val	His	Tyr	Asp	Ser	Asp	Ser	Tyr	Asp	Ser	Leu	Ser	Glu	Ala
				140					145					150
Ala	Glu	Arg	Pro	Gln	Gly	Leu	Ala	Val	Leu	Gly	Ile	Leu	Ile	Glu
				155					160					165
Val	Gly	Glu	Thr	Lys	Asn	Ile	Ala	Tyr	Glu	His	Ile	Leu	Ser	His
				170					175					180
Leu	His	Glu	Val	Arg	His	Lys	Asp	Gln	Lys	Thr	Ser	Val	Pro	Pro
				185					190					195
Phe	Asn	Leu	Arg	Glu	Leu	Leu	Pro	Lys	Gln	Leu	Gly	Gln	Tyr	Phe
				200					205					210
Arg	Tyr	Asn	Gly	Ser	Leu	Thr	Thr	Pro	Pro	Cys	Tyr	Gln	Ser	Val
				215					220					225
Leu	Trp	Thr	Val	Phe	Tyr	Arg	Arg	Ser	Gln	Ile	Ser	Met	Glu	Gln
				230					235					240
Leu	Glu	Lys	Leu	Gln	Gly	Thr	Leu	Phe	Ser	Thr	Glu	Glu	Glu	Pro
				245					250					255
Ser	Lys	Leu	Leu	Val	Gln	Asn	Tyr	Arg	Ala	Leu	Gln	Pro	Leu	Asn
				260					265					270
Gln	Arg	Met	Val	Phe	Ala	Ser	Phe	Ile	Gln	Ala	Gly	Ser	Ser	Tyr
				275					280					285
Thr	Thr	Gly	Glu	Met	Leu	Ser	Leu	Gly	Val	Gly	Ile	Leu	Val	Gly
				290					295					300
Cys	Leu	Cys	Leu	Leu	Leu	Ala	Val	Tyr	Phe	Ile	Ala	Arg	Lys	Ile
				305					310					315
Arg	Lys	Lys	Arg	Leu	Glu	Asn	Arg	Lys	Ser	Val	Val	Phe	Thr	Ser
				320					325					330
Ala	Gln	Ala	Thr	Thr	Glu	Ala								
				335										

<210> 424
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 424
 gtaaagtcgc tggccagc 18

<210> 425
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.

<400> 425
 cccgatctgc ctgctgta 18

<210> 426
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 426
 ctgcactgta tggccattat tgtg 24

<210> 427
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 427
 cagaaaccca tgatacccta ctgaacaccg aatccccctgg aagcc 45

<210> 428
 <211> 1073
 <212> DNA
 <213> Homo sapiens

<400> 428
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 acatttttgcc tcgtggaccc aaaggtagca atctgaaaca tgaggagtac 100
 gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150

<220>
<223> Synthetic oligonucleotide probe

<400> 440
gggtcgtgtt ttggagaga 19

<210> 441
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 441
ctggccctca gagcaccaat 20

<210> 442
<211> 25
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 442
tcctccatca cttcccctag ctcca 25

<210> 443
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 443
ctggcaggag ttaaagttcc aaga 24

<210> 444
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
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<400> 444
aaaggacacc gggatgtg 18

<210> 445
<211> 26
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<220>
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<400> 445
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<210> 446
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<212> DNA
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<220>
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<400> 446
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<210> 447
<211> 20
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<220>
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<400> 447
  caggactgag cgcttggtta 20

<210> 448
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<220>
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<400> 448
  caaagcgcca agtaccggac c 21

<210> 449
<211> 18
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<220>
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<400> 449
  ccagacctca gccaggaa 18

<210> 450
<211> 18
<212> DNA
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<220>
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<400> 450
  ccctagctga ccccttca 18

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<210> 451
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 451
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<210> 452
<211> 26
<212> DNA
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<220>
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<400> 452
ctctccccct cccttttctt ttgttt 26

<210> 453
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<220>
<223> Synthetic oligonucleotide probe

<400> 453
ctctggtgcc cacagtga 18

<210> 454
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 454
ccatgcctgc tcagccaaga a 21

<210> 455
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<220>
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<400> 455
caggaaatct ggaaacctac agt 23

<210> 456
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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 456

ccttgaaaag gaccagttt 20

<210> 457

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 457

atgagtcgca cctgctgttc cc 22

<210> 458

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 458

tagcagctgc ccttggtta 18

<210> 459

<211> 22

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<223> Synthetic oligonucleotide probe

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<210> 460

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 460

tgctaggcga cgacacccag acc 23

<210> 461

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 461

tggaacacgtg gcagtgga 18

<210> 462

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 462

tcatgggtctc gtccattc 19

<210> 463

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 463

caccatttgt ttctctgtct ccccatc 27

<210> 464

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 464

ccggcatcct tggagtag 18

<210> 465

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 465

tccccattag cacaggagta 20

<210> 466

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 466

Sequence = 5' to 3'

aggctcttgc ctgtcctgct gct 23

<210> 467

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 467

gcccagagtc ccacttgt 18

<210> 468

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 468

actgctccgc ctactacga 19

<210> 469

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 469

aggcatcctc gccgtcctca 20

<210> 470

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 470

aaggccaagg tgagtccat 19

<210> 471

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 471

cgagtgtgtg cgaaacctaa 20

<210> 472

<211> 24
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<220>
 <223> Synthetic oligonucleotide probe

<400> 472
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<210> 473
 <211> 19
 <212> DNA
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<220>
 <223> Synthetic oligonucleotide probe

<400> 473
 aaggccaagg tgagtccat 19

<210> 474
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<220>
 <223> Synthetic oligonucleotide probe

<400> 474
 cctactgagg agccctatgc 20

<210> 475
 <211> 22
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<220>
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<400> 475
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<210> 476
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 476
 gggaggctta taggcccaat ctgg 24

<210> 477
 <211> 50
 <212> DNA
 <213> Artificial Sequence

$\langle 220 \rangle$

<223> Synthetic oligonucleotide probe

<400> 477

ggcttcagca gcacgtgtga agtcgaagtc gcagtcacag atatcaatga 50

Variable	Mean	SD	Min	Max
Age	34.5	10.2	20	55
Gender	50.0	50.0	0	100
Marital status	65.0	48.0	0	100
Education	12.5	1.5	9	16
Income	3500	1500	1000	8000
Occupation	2.5	1.5	1	5
Health status	75.0	25.0	50	100
Stress level	60.0	20.0	40	80
Life satisfaction	70.0	20.0	50	90
Resilience	65.0	25.0	40	90
Optimism	75.0	20.0	50	90
Self-efficacy	70.0	25.0	40	90
Emotional stability	60.0	20.0	40	80
Neuroticism	30.0	15.0	10	50
Extraversion	50.0	20.0	30	70
Conscientiousness	60.0	20.0	40	80
Agreeableness	55.0	20.0	35	75
Openness	45.0	20.0	25	65
Depression	20.0	10.0	0	40
Anxiety	25.0	10.0	0	40
Loneliness	30.0	10.0	0	40
Isolation	15.0	5.0	0	30
Support	70.0	20.0	50	90
Helpfulness	60.0	20.0	40	80
Empathy	65.0	20.0	45	85
Compassion	60.0	20.0	40	80
Kindness	65.0	20.0	45	85
Generosity	60.0	20.0	40	80
Altruism	65.0	20.0	45	85
Cooperativeness	60.0	20.0	40	80
Teamwork	65.0	20.0	45	85
Leadership	60.0	20.0	40	80
Communication	65.0	20.0	45	85
Interpersonal skills	60.0	20.0	40	80
Conflict resolution	65.0	20.0	45	85
Problem solving	60.0	20.0	40	80
Decision making	65.0	20.0	45	85
Goal setting	60.0	20.0	40	80
Time management	65.0	20.0	45	85
Organization	60.0	20.0	40	80
Productivity	65.0	20.0	45	85
Efficiency	60.0	20.0	40	80
Effectiveness	65.0	20.0	45	85
Success	60.0	20.0	40	80
Accomplishment	65.0	20.0	45	85
achievement	60.0	20.0	40	80
Realization	65.0	20.0	45	85
Fulfillment	60.0	20.0	40	80
Meaning	65.0	20.0	45	85
Purpose	60.0	20.0	40	80
Direction	65.0	20.0	45	85
Clarity	60.0	20.0	40	80
Focus	65.0	20.0	45	85
Concentration	60.0	20.0	40	80
Attention	65.0	20.0	45	85
Alertness	60.0	20.0	40	80
Awareness	65.0	20.0	45	85
Insight	60.0	20.0	40	80
Understanding	65.0	20.0	45	85
Knowledge	60.0	20.0	40	80
Wisdom	65.0	20.0	45	85
Intelligence	60.0	20.0	40	80
Reasoning	65.0	20.0	45	85
Logic	60.0	20.0	40	80
Analysis	65.0	20.0	45	85
Synthesis	60.0	20.0	40	80
Evaluation	65.0	20.0	45	85
Judgment	60.0	20.0	40	80
Discernment	65.0	20.0	45	85
Perception	60.0	20.0	40	80
Observation	65.0	20.0	45	85
Attention	60.0	20.0	40	80
Focus	65.0	20.0	45	85
Concentration	60.0	20.0	40	80
Alertness	65.0	20.0	45	85
Awareness	60.0	20.0	40	80
Insight	65.0	20.0	45	85
Understanding	60.0	20.0	40	80
Knowledge	65.0	20.0	45	85
Wisdom	60.			